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390
                                                            SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATY 240
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                                                                                                                                                                                                      KRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKBEHLDVASPDKASSP 480
                                                                                                                                                                                                                   631 KRIPPIKTRPLKGGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSP 690
                                     CKVILLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPROGRNDIELTPPKGYEAQTFNW
                                                                                                         CXVLLDGYLMICVDGGPSTDGLDWFCXHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW
                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lethal(3)malignant brain tumor-like 2 protein (L(3)mbt-like 2 protein)
(H-1(3)mbt-like protein).
                          VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM
                                                                          391 SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPINLGNICVATV
                                                                                                                                  ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF
                                                                                                                                            maintain the transcriptionally repressive state of genes, probably via a modification of chromatin, rendering it heritably changed in
                                                                                                                                                                     DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKBATKKKKKQFGKKR
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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P59178;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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complex suggests that it may contribute to prevent expression of genes that trigger the cell into mitcsis (By similarity).

-! SUBURIT: Part of the E2F6.com-1 complex in G0 phase composed of E2F6, MGA, MAX, TFDP1, EAR3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, BAT8 and YAP2 (By similarity).

-! SUBCEDILIVAR LOCATION: Nuclear (Probable).

-! SIMILARITY: Contains 1 C4-type zinc finger.

-! SIMILARITY: Contains 4 MBT domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKVLLDGYLMI CVDGGPSTDGSDWFCYHASSHAI FPATFCQKNDI ELTPPKGYETQPFAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            process, marking Chromatin regulator; Nuclear protein; nger; Metal-binding; Repeat. 90 114 C4-TYPE.
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89.7%; Pred. No. 1.6e-195;
iive 23; Mismatches 26;
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POLY-LYS.
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MBT 3.
MBT 4.
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MGD; MG1:2443584; 4732493N06Rik.
SMART; SN00561; MBT; 4.
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Zinc-finger; M
ZN_FING 9
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QFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDVA
SPDKASSPELPVSVENIKQETDD"
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99.9%; Score 2553.4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2554; Conservative 0; Mismatches
                   /gene="H-1(3)mbt-like"
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/gene="H-1(3)mbt-like
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Homo sapiens mRNA for H-l(3)mbt-like protein, alternative variant
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Submitted (25-37M-2001) Wismar J., Johannes Gutenberg Universitaet,
Institut fuer Genetik, Becherweg 32, 55099 Mainz, GERMANY
Location/Qualifiers
1. 3134
/ organism="Homo sapiens"
/ mol_type="mRNA"
/ db_xref="taxon:9606"
/ chromosome="122"
/ map="22q13.31-33"
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AJ305226.1 GI:13940238
alternative splicing; H-l(3)mbt-like gene; H-l(3)mbt-like protein.
Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                GACAGTGAGTTGTGTGGTGGGGGGGAGCCTCTGCCTCAAAAATTCACCAAGCAGAATGCCT
                                             1981 GACAGTGAGTTGTGTGGGGGGGGGCGCCTCTGCCTCAAAAATTCACCAAGAATGCCT
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Molecular characterization of h-l(3)mbt-like: a new member of
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FEBS Lett. 507 (1), 119-121 (2001)
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Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Brand P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Brands R.L., Fey J.M., Crafham D.V., Griffiths M.N.D., Hall C., Garner A.A., Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimperley A.M., King A., Laird G.K., Langford C.F., Kershaw J., Kindlerley A.M., King A., Laird G.K., Dangford C.F., Kershaw J., Milne S.A., Milne S.A., Motlaren S., Modlaren S., Motlaren S., Motlaren S., Modlaren S., Motlaren S., Modlaren S., Motlaren S., Modlaren S., Modlaren S., Modlaren S., Modlaren S., Modlaren S., Modlaren S., Motlaren S., Modlaren S., Motlaren S., Modlaren S., Modlaren S., Modlaren S., Modlaren S., Sanlay H., Ramsey Y., Rages D., C.T., Soctt C.E., Sehra H.K., Succe C.D., Smalley S., Smith M.L., Steward C.A., Sulston J.B., Swann R.M., Walliams L., Williams L., Williams S., Shawasaki K., Sasaki T., Asakawa S., Sudoh J., Shimizu M., Shibuya K., Soshizaki Y., Aoki W., Willey D., John A., Do T., Dorman A., Shibuya K., Soshizaki Y., Asakawa S., Kudoh J., Song L., Morman A., Eang F., Fu Y., Hu P., Hua A., Kencon S., Lai H., Bourne S., Lai S., Otan Y., Wang Z., White J., Williams D., Wu H., Soog Z., Mang Q., Wang Y., Wang Z., White J., Williams D., Graves T., Hawkins J., Mang C., Wang S., Luton R., Johnson D., Bemis G., Mang Y., Wang X., White W., Modlamn D., Graves T., Hawkins J., Andrew M., Milliams M., Waller K., Kenper K., Latreille P., Layman D., Ozersky P., Rodet P., Malker C., Wangley A., Worden D., Satta S., Bader M., Milliams D., Williams D., Warder C., Worley D., Benis G., Worrow B.E., Edelmann L., Robernand H.E., Johnson A., Wong A.C.C., Worrow B.E., Edelmann L., Millianson P., Bodented H., Word P., Walley
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WEDINE=22188257; PubMed=12477932;

WEDINE=22188257; PubMed=12477932;

RIAUSERER R.D., Colling F.G., Wagner L., Shemmen C.M., Schuler G.D.,

A Klausner R.D., Colling F.G., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Carmen G.M., Robertz T.E.,

A Rapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

A Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Galbbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R. Hotriger A.C., Grimwood J., Schmutz J., Marra M.A.,

Butterfield Y.S. N., Krzywinski M.I. Skalska U., Smallus D.E.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Furnar L. Contant M. Schein J.E., Jones S.J.M., Marra M.A.,

R. Chenerch A., Schein J.E., Jones S.J.M., Marra M.A.,

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R. Chenerch A., Schein J.E., Grimce T. S.D. Grimce T. S
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RING1; RNF2; MBLR; BAT8 AND YAF2.
MEDLINE=21999559; PubMed=12004135;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
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C4-TYPE. Missing 705 AA; 79110 MW; HGNC:18594; L3MBTL2 Name=1; Synonyms=A; 300 617 705 618 300 608 615 Polymorphism, ZN FING 9 DOMAIN 21 SEQUENCE VARSPLIC VARSPLIC ARSPLIC VARSPLIC VARIANT DOMAIN NIAMOC DOMAIN DOMAIN DOMAIN Ogawa H., Ishiguro K.-I., Gaubatz S., Livingston D.M., Nakatani Y.;
"A complex with chromatin modifiers that occupies B2F- and
Myc-responsive genes in G0 cells.";
Science 296:1132-1136(2002)
-!- FUNCTION: Putative Polycomb group (PcG) protein. PcG proteins
maintain the transcriptionally repressive state of genes, probably
via a modification of chromatin, rendering it heritably changed in
its expressibility. Its association with a chromatin remodeling

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 211 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI 270 1 MKGMKVBVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI 60 -i- CAUTION: Ref.3 sequences differ from that shown in that they seem to include introlic sequence. -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous gene model prediction. Query Match
100.0%; Score 2683; DB 1; Length 705;
Best Local Similarity 100.0%; Pred. No. 3.8e-216;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps Missing (In isoform 2). /FTIG=VSP 003905. EPATPLKAXE -> GVGSRGPKRL (in.isoform 3). complex suggests that it may contribute to prevent expression of genes that trigger the cell into mitosis. E2F6, MGA, MAX, TFDF1, CHX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, BAT8 and YAF2. GK; Q969R5; -.
InterPro; IPR04092; Mbt.
Pfam; PF02820; mbt; 4.
SWART; SW00561; MBT; 4.
Transcription regulation; Chromatin regulator; Nuclear protein; Zinc-finger; Metal-binding; Repeat; Alternative splicing; POLY-GLU. DOLY-LAS. EPATIMEN -> GKLPRSL (in isoform 2). /FTId=VSP_003904. Name=2; Synonyms=B; IsoId=0969R5-2; Sequence=VSP_003904, VSP_003905; IsoId=0969R5-3; Sequence=VSP_003906, VSP_003907;
-!- SIMILARITY: Contains 1 C4-type_zinc finger.
-!- SIMILARITY: Contains 4 MBT domains. /FTId=vSP_003906. Missing (in isoform 3). /FTId=vSP_003907. R -> W (IN dbSNP:2277846) FTId=VAR_015093. 8FC86A440982FFA7_CRC64; Event=Alternative splicing; Named isoforms=3; -!- SUBCELLULAR LOCATION: Nuclear (Probable). IsoId=Q969R5-1; Sequence=Displayed; EMBL, AJ305226; CAC37794.1; -.
EMBL, AJ305227; CAC37795.1; -.
EMBL, AL136564; CAB66499.1; -.
EMBL, AKO74091; BAB84917.1; ALT_SEQ.
EMBL, AKO77052; BAC04936.1; ALT_SEQ.
EMBL, AL035681; -; NOT_ANNOTATED_CDS.
EMBL, AL035681; CAB63071.1; ALT_SEQ.
EMBL, BC017191; AAH17191.1; -. /FTId=VAR genes that trigger the cell--!- SUBUNIT: Part of the E2F6.c a à

61 GWCAINSŘÍLVPPRTIHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE 120

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 4, 2004, 09:05:51; Search time 18 Seconds (without alignments) 1293.234 Million cell updates/sec

US-10-031-915-36 2683 1 MKGMKVEVLANSDAVLPSRVY......KASSPELPVSVENIKQETDD 495 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues

127863 Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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* Query Match	. 0	0	19.0	4.5	4.3	4.1	3.9	3.7	3.7	3.6	3.6	3.4	3.4	3.4	3.4	3.4	3.4	3.4		3.3						٠		•	•	•	3.5	3.2	3.2
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JAKI_CYPCA TOPI_CANGA SYEP_HUMAN SYEP_HUMAN SYA_THEVO FD12_MORIS PRP2_KABLA NUCD_BUCAI GLMS_PYRAE PPCK_HABCO NFC3_HUMAN MAPB_HUMAN	
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ALIGNMENTS

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661 GAGCAGTCTRACACAGAGGGGGTTGGTTTGAGGAAGGGGATGAACTGGAGGCCATTGACC 1295 GAGCAGTCTRACACAGAGGGGGTTGGTTTGAGGAAGGGATGAACTGGAGGCCATTGAC 1295 GAGCAGTCTRACACAGAGGGGTTGGTTTGAGGAGAGGGTTGATTGAGGATCTCTGGAGGCCATTGAC 1295 GAGCAGTCTACACAGAGGGTTGGTTTGAGGAGGGATTGATCTGGAGGGTTCCT 1295 GAGCAGTCTGACAGAGGGAACTGTTGTAGAGGTTCTCTGGAGGATCACTCTTGAGGTTCCT 1296 GAGCAGTTGAGAGGGAACTGCTGCAGAGGATTGATCTGGACGATCACTCT 1297 TATTAATCTGGGCAACTGTGCAGATGGTTTGAACTGGACTGGTTCTGTAACTCACAC 1297 CCTCTTCCCCACCCCATTGTGAACTGGTTCTGAACTGGTTCTGTAACTCACAC 1297 CCTCTTCCCCACCCCATTGTGAACTGGTTCTGAACTGGTTCTGTAACTCACAC 1297 CCTCTTCCCCACCCCATTGTGAACTGGTTCTGTAACTCACACTGTTCTGTAACTCACAC 1297 CCTCTTCCCCACCCCATTGTTGAACTGGTTCTGTAACTCACACACA	1501

us-10-031-915-36.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 4, 2004, 09:05:51 ; Search time 18 Seconds (without alignments) 1293.234 Million cell updates/sec

US-10-031-915-36 2683 1 MKGWKVEVLNSDAVLPSRVYKASSPELPVSVENIKQETDD 495 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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86	98	98	85.5	85.5	82	82	82	82	82	82	82	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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RA Conroy D., Corby N.R., Ceville G.J., Cox A.V., Davis J., Dawson E., Brans P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Blington A.G., Aller J.G., Goward M.E., Caratham D.V., Griffiths M.N.D., Hall C., R. Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S., Holmes S., Hant S.E., Jones M.C., Kershaw J.Y., Kimberley A.M., King A., Laird G.K., Langford C.F., Leversia M.A., Lloyd C., Lloyd D.M., Rarty J., Mclaren S., McMurray A.A., Mille S.A., Mortimore B.J., Mclaren S., McMurray A.A., Mille S.A., Mortimore B.J. C.T., R. Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Skott C.E., Spragon L., Steward C.A., Sulston J.E., Swann R.M., Williams S.A., Williams S.A., Williams S.A., Williams S.A., Williams D.L., Williams S.A., Milliams S.A., Williams S.A., Williams S.A., Williams S.A., Shibuya K., Sasaki T., Aski W., Mitsuyama S., Rober B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., R.A. Dorman A., Shibuya K., Yongi T., Hua A., Kanton S., Lait H., Lao H., R. Ang Q., Mang Y., Hu P., Waltaj E., Walten T., Bentley D., Shaull S., Sloan D., Song L., R. Ang Q., Mang Y., Hu P., Walte B., Multing T., Lewis S., Lin S.-P., Loh P., Malaj E., Mutray J., Miller M., Miller M., Milson R., Annoshima H., Shang G., Mutray J., Miller M., Mank P., Cordes M., De S., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., R. Annoshim H. E., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Korf I., Bedell J.A., Hillier L., Warter S., Worrew B.E., Edelmann L., Korfer D., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., Karnson H., Wander C., Warrey J.P., Peyrard M., Kern S., Shaikh T., Kurahashi H., Saitta S., Budarf M., Shaikh H. S., Shaikh T., Mutrahashi H., Saitta S., Budarf M., Shinan D., Shaikh T., Martin B., Peyrard M., Walkinson P., Bodentelich A., Warrey D., Peyrard M., Peyrard M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilkinson P., Bodenteich A., Hartman K., Hu
Tilahun Y., Wright H.;
"The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

NENGLY REPER AND YAFE.

RENGLY, RNEF, MARK, BATE AND YAFE.

MEDLINE-21999559, PubMed=12004135,

MEDLINE-21999559, PubMed=12004135,

Gawa H., Ishiguro K.-I., Gaubatz S., Livingston D.M., Nakatani Y.,

"A complex with chromatin modifiers that occupies E2F- and

Myc-responsive genes in G0 cells.",

Science 296:1132-1136(2002)

-I- FUNCTION: Putative Polycomb group (PcG) protein. PcG proteins

maintain the transcriptionally repressive state of genes, probably

via a modification of chromatin, rendering it heritably changed in

its expressibility. Its association with a chromatin remodeling

GWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE 120

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 211 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHP1 270 09 /FILG=VSP_00390'.
/FILG=VSP_00390's.
/FILG=VSP_003905.
RPATPLEAKE -> GGGSRGPKRL (in isoform 3).
/FILG=VSP_003906.
Missing (In isoform 3).
/FILG=VSP_003907.
/FILG=VSP_003907.
/FILG=VSP_015093. IsoId=0969R5-3; Sequence=VSP 003906, VSP 003907;
-!- SIMILARITY: Contains 1 C4-type_zinc finger.
-!- SIMILARITY: Contains 4 MBT domains.
-!- CAUTION: Ref.3 sequences differ from that shown in that they seem 1 MKGMKVBVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI Gaps complex suggests that it may contribute to prevent expression of genes that trigger the cell into mitosis.
SUBUNIT: Part of the E2F6.com-1 complex in G0 phase composed of E2F6.MGA, MAX, TFDP1, CBX3, BAT8, EURMTASEL, RING1, RNF2, MBLR, to include intronic sequence.
-!- CAUTION: Ref.4 sequence differs from that shown due to erroneous gene model prediction. MBT 1. MBT 2. MBT 3. MBT 4. POLY GLU. POLY - IXS. EPATPIK -> GKLPRSL (in isoform 2). /FIId=VSP_003904. Transcription regulation; Chromatin regulator; Nuclear protein; Zinc-finger; Metal-binding; Repeat; Alternative splicing; .. 100.0%; Score 2683; DB 1; Length 705; ilarity 100.0%; Pred. No. 3.8e-216; Conservative 0; Mismatches 0; Indels 0; /FTId=VAR_015093. 705 AA; 79110 MW; 8FC86A440982FFA7 CRC64; Name=2; Synonyms=B; IsoId=2969R5-2; Sequence=VSP_003904, VSP_003905; Event=Alternative splicing; Named isoforms=3; SUBCELLULAR LOCATION: Nuclear (Probable). ALTERNATIVE PRODUCTS: Name=1; Synonyms=A; IsoId=Q969R5-1; Sequence=Displayed; EMEL, AL136564; CAB66499.1; -..
EMEL, AK074091; BAB84917.1; ALT. SEQ.
EMEL, AK097052; BAC04936.1; ALT. SEQ.
EMEL, AL03568; -; NOT ANNOTATED CDS.
EMEL, AL035681; CAB63071.1; ALT. SEQ.
EMEL, BC017191; AAH7191.1; -..
Genew, HGNC:18594; L3MBTL2. C4-TYPE. EMBL; AJ305226; CAC37794.1; -. EMBL; AJ305227; CAC37795.1; -. InterPro; IPR004092; Mbt. Pfam; PF02820; mbt; 4. SMART; SMO0561; MBT; 4. 300 617 705 Query Match Best Local Similarity Matches 495; Conserv and YAF2 300 540 17 620 608 618 615 609 GK; Q969R5; InterPro; IPE Polymorphism Name=3 SEQUENCE MRSPLIC VARSPLIC MARSPLIC MARSPLIC VARIANT DOMAIN DOMAIN DOMAIN DOMAIN 111 셤 à

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-Chal(3)malignant brain tumor-like 2 protein (L(3)mbt-like 2 like 3 like 3
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SUBUNIT: Part of the 2F6.com-1 complex in GO phase composed of E2F6, MGA, MAX, TFDP1, CBX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, SUBCELLUIAR LOCATION: Ordear (Probable).

SUBCELLUIAR LOCATION: Nuclear (Probable).

SIMILARITY: Contains 1 C4-type zinc finger. Gaps MGD; MGI:2443584; 4732493NG6Rik.
SMART; SM00561; MBT; 4.
Transcription regulation; Chromatin regulator; Nuclear protein;
Zinc-finger; Metal-binding; Repeat.
ZN FING 214 291 MBT 1.
MBT 1. .. Length 703; Indels 2E9B5DF5BFDAAEB9 CRC64; 90.8%; Score 2436; DB 1; 89.7%; Pred. No. 1.6e-195; ive 23; Mismatches 26; ELPVSVENIKQETDD 495 :||::|:|||| :: QLPLPIESIKQERNN 703 631 481 g ઠે à

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DESIGNATION OF STRUMED: PRT: 772 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARIVEVITYSEGKTLUWITYAQLGDLVCSDHLOEGKGILETGV
HSLLCSLPTHLLAKLSFASDSQY -> VRCKCRVGDRAGVT
VLKTAGSRCPPQRHFC (in isoform 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARIVRVTHVSGKTLVWTVAQLGDLVCSDHLQEGKGILETGV
HSLLCSLPTHLLAKLSFASDSQY -> MIDGEAFLLLTQAD
                                                                                                                                                                                                Isold=03Y468-4; Sequence=VSP 003903; ISSUE SPECIFICITY: Widely expressed. Expression is reduced in colorectal cancer cell line SW480 and promyelocytic leukemia cell
                                                                                                                                                                                                                                                                                                                       -!- SIWILARITY: Contains 3 mbt domains.
-!- CAUTION: Ref.3 (CAC18508) sequences differ from that shown due to
erroneous gene model prediction.
required to accomplish normal mitosis.

SUBCELLUIAR LOCATION: Nuclear; excluded from the nucleolus. Does not colocalize with the PCG protein BMI1, suggesting that these two proteins do not belong to the same complex.

ALTERNATIOE PRODUCTS:

Bythermative splicing; Named isoforms=4;

Name=1; Synonyms=mbt-1;

Isode@97468-1; Sequence=Displayed;

Name=2; Synonyms=mbt-1i;

Isode@97468-2; Sequence=VSP_003902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSLLCSLPTHLLAKLSFASDSQY -> MIDGBAF;
IVKIMSVKLGPALKIYNAILMFKNADDTLK (in
                                                                                                                                                                                                                                              line HL-60.
DEVELOPMENTAL STAGE: In interphase cells, it is scattered throughout the nucleoplasm. In mitotic cells, it strongly associates with condensed chromosomes from the prophase to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromatin regulator; Zinc-finger;
ein; Repeat; Alternative splicing.
MBT 1.
MBT 2.
MBT 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform 4).
/FTId=VDB 003903.
/FTId=VDB 003903.
LR -> MC (IN REF. 1).
L -> M (IN REF. 1).
L -> M (IN REF. 1).
K -> P (IN REF. 1).
W, 117B03A628826829 CRC64;
                                                                                                                                                      Name=3;
IsoId=09Y468-3; Sequence=VSP_003901, VSP_003902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 3). /FIId=VSP 003901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  003902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U89358; AAC69438.1; -.
EMBL; AL110279; CAB33714.1; -.
EMBL; 298752; CAC16799.1; -.
EMBL; 298752; CAC16800.1; -.
EMBL; AD931691; CAC18508.1; -.
EMBL; AL031681; CAS43959.1; -.
EMBL; AL011681; CAS43959.1; -.
EMBL; AB014581; BAA31656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform 3)
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315 MB
422 MB
526 MB
578 C2
348 Mi
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321 LR
332 L
595 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02820; mbt; 3. Pfam; PF01530; zf-C2HC; 1. SMART; SM00561; MBT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:15905; L3MBTL.
GK; Q9Y468; -.
InterPro; IPR004092; Mbt.
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DNA-binding; Nuclear prote
DOMAIN 242 315
DOMAIN 349 422
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595
772 AA;
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161 WSPLIHPV----GWSRRVGHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGG 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO126; FASEC_1; 1.
PROSITE; PSO1286; FASEC_1; 1.
PROSITE; PSO1226; FASEC_2; 1.
PROSITE; PSO5022; FASEC_3; 1.
PROSITE; PSO5006; LDLMA_1; 3.
PROSITE; PSO5006; LDLMA_2; 3.
PROSITE; PSO508; TSP1; 4.
PROSITE; PSO184; VWFC_2; 1.
Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
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TESP TYPE-1 4.

BY SIMILARITY.

BY SIMILARITY.
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20.8%; Pred. No. 0.041;
ive 38; Mismatches 130; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91817 MW; 9538F2108E787B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444
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LDL-RECEPTOR CLASS A
LDL-RECEPTOR CLASS A
LDL-RECEPTOR CLASS A
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EGF-LIKE 1.
EGF-LIKE 2.
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VWFC.
                    or send an email to license@isb-sib.ch)
                                                                                                          HASEP, TALLAU, TANDO.

INCERPRO, INCO0421; FASB C.

INCERPRO; IPRO0219; ILL FECEDTOR.

INCERPRO; IPRO0219; ILL CYBRICH.

INCERPRO; IPRO0108; VWF C.

Pfam; PF00186; FS FB LYPE C; I.

Pfam; PF00187; INL TECEPT A; 3.

Pfam; PF00187; INL 1.

SWART; SW00231; PASBC; 1.

SWART; SW00209; INL 1.

SWART; SW00209; INL 1.

SWART; SW00209; INL 1.
                                                   EMBL; X93922; CAA63815.1; -.
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                                                                                                                                               141 GRIRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSE--RRSDMAHHPTFRKIYC 198
                                                                                                                                                                                                                                                         199 DAVP-YLFKKVRAVYTEGGWFEEGWKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGP 257
                                                                                                                                                                                                                                                                                                                                                                   326 QAAPKHLFVSQSHSPPPLG-FQVGMKLEAVDRMNPSLVCVASVTDV-VDSRFLVHFDNWD 383
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGY-EAQTFNWENYLEKTKSKAAPSRL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DI--YDYWC-DPSSPYIHPVGWCQKQKPLTPPQDYPDPDNFCWEKYLEETGASAVPTWA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIYPVGWCELTGYQLQPPVA-AEPAT-----PLKAKEATKKKKKQFGKKRKRIP---- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESP 376
                                                                                                               83 WKGYLMKRLVGSRTLPVDF--HIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVVDTVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Ependymocyte,
MEDLINE=96338614; PubMed=8743952;
GODDINE=96338614; PubMed=8743952;
GODDINE=96338614: Mennellel R., Creveaux I., Lehmann W.,
Lamalle D., Dastugue B., Meinhel A.;
"SCO-spondin: a new member of the thrombospondin family secreted by the subcommissural organ is a candidate in the modulation of neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last annotation update)
SCO-spondin (Fragment)
Bos taurus (Bovine)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggregation...;

1. Call Sci. 109:1053-1061(1996)...

-1. FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION...

-1. STBCELLULAR LOCATION: Extracellular...

-1. TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN...

-1. DEVELLOPMENTAL STAGE: BNBRYO...

-1. SIMILARITY: COLLAINS at 1east 4 TSP type-1 domains...

-1. SIMILARITY: Contains at least 2 EGF-like domains...

-1. SIMILARITY: Contains at least 1 F5/8 type C domain...

-1. SIMILARITY: Contains at least 3 LDL-receptor class A domains...

-1. SIMILARITY: Contains at least 3 LDL-receptor class A domains...

-1. SIMILARITY: Contains at least 3 LDL-receptor class A domains...

-1. SIMILARITY: Contains at least 3 LDL-receptor class A domains...
  19.0%; Score 510; DB 1; Length 772;
33.7%; Pred. No. 1.2e-34;
Live 53; Mismatches 168; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 DGSGHVTGKFTAHHCLSGCPLAER--NÓSRLKAELSDSEASARK 601
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                                                            Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Query Match
Best Local Similarity
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P98167;
                                                                                                                                                                                                                                                                                                                                                                                                                                           258
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SSPO BOVIN
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NCBI_TaxID=9606;
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                      -- QAAPSSDAN 490
                                                                       364
                                                                                                                                                                                                    IPPIKTRPLROGSKKPLLEDDPQGARKISSEPVPGBIIAVRVKEEHLDVASPDKASSPEL 482
                                                                                                                                                                                                                                                                                        LDGP-----LRVELLG-CEPAPLCLG----VGHRCVSGECAPRGAPCDGVEDCKDGSD 538
                                                                                                                                                                  SEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEATKKKKKQFGK--KRKR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C., Science 270:397-403(1995).
                                                                    MDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF--------DGWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma genitalium.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 200;
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4.3%; Score 116.5; DB 1, Length 2
Best Local Similarity 25.0%; Pred. No. 0.014;
Matches 44; Conservative 38; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 50S RIBOSOMAL PROTEIN L29.
200 UNKNOWN.
23258 MW; 5EC115E52AA5EA92 CRC64;
: | | : : | | : : | 446 APQLFPKNWNGPSTVWMFARWVQARHVRVWPSDGHH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Sols ribosomal protein L29.
RPMC OR RPL29 OR MG159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP, MF_00374; fused; 1.
InterPro; IPR001854; Ribosomal L29.
Pfam, PF00831; Ribosomal_L29; 1.
TGRPAMS; TIGR00012; L29; 1.
PROSITE; PS00579; RIBOSOMAL_L29; 1.
Ribosomal protein; 7, 7, 508 RIBOSOMALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U39696; AAC71377.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
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SEQUENCE
                                                                       319
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MYCGE
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331 KLEAVDLMEPRLICVATVKRVVHRLLSIHFD---GWDSEYDQW--VDCESPDIYPVGW-- 383

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                                                                 90 KLSTKPESKQETKKAEVFKVESKPESKQETKKAEVKPLKQETKKVEVKPKVEPKPLKQE 149
                                           434
32 KLAHGELDKPHLI--AKVRKLLAVVIJILTERKLNWQVEKDKYKLLSRKTNELIVNSWKQ 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gergely F., Karlsson C., Still I.H., Cowell J.K., Kilmartin J., Raff J.W.,
                                         -----CELTGYQLQPPVAAEPATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQG
                                                                                                                       435 SKKPLLEDDPQGARKISSEPVPGEIIAVRVKŒEHLDVASPDKASSPELPVSVENIK 490
                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAX PLAX A ROLE IN ORGANIZING CENTROSOWAL MICROTUBULES.
MAY ACT AS A TUMOR SUPPRESSOR PROTEIN. MAY REPRESENT A TUMOR PROGRESSION MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 44-1026 FROM N.A. (ISOFORM 3).
Pu J., Li C., Rodriguez M., Banerjee D.;
"Expression of TACC2 protein mRNA in human microvascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20214826; PubMed=10749935;
Chen H. M., Schmeichel K.L., Mian I.S., Lelievre S., Petersen O.W.,
Bissell M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      candidate breast tumor suppressor and biomarker for tumor
                                                                                                                                                                                                                                                                TAC2_HUMAN STANDARD; PRT; 1026 AA.
095359; Q9NZ41; Q9NZR5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transforming acidic coiled-coil-containing protein 2 (Anti Zuai-1)
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: INTERECTS WITH MICROTUBULES.
-!- SUBCELLUTAR LOCATION: NUCLEAR; CONCENTRATED AT CENTROSOMES.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=3; Comment=Experimental confirmation may be lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=095359-2; Sequence=VSP_006368, VSP_006369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97:14352-14357(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Brain, Fetal brain, and Skeletal muscle;
MEDLINE=20570483; PubMed=11121038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 375-1026 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOId=095359-3; Sequence=VSP 006369; SIMILARITY: BELONGS TO THE TACC FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=095359-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Cell 11:1357-1367(2000).
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Genomics 2:249-256(1988)
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     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 VDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 ------DAKNQEGKVNTRRKSTD-----SVPISKSTLSRSLSLQASDFDGASSGNP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 -PTETPPVKETQQEP----DEESL-----VPSGENLASETKTESAKTEGPSPALLEET 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 PSRLFNWDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIH---FDGWDSEYDQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 PPTKTRPLROGSKKPLLEDDPQGARKISSEPVP-GELIAVRVKEEHLDVASPDKASSPEL 482
                                                                                                                                                                                                                          370 WVDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEATKK-----KKKQFGKKRKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Gaps
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Zeviani M., Darras B.T., Rizzuto R., Salviati G., Betto R.,
Bonilla E., Miranda A.F., Du J., Samitt C., Dickson G., Walsh F.S.,
Dimauro S., Francke U., Schon E.A.;
"Cloning and expression of human nebulin cDNAs and assignment of the
gene to chromosome 2g31-q32.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Labeit S., Kolmerer B.; "The complete primary structure of human nebulin and its correlation
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%; Score 109.5; DB 1; Length 1026; 23.6%; Pred. No. 0.47; ative 33; Mismatches 95; Indels 57;
                                                                                                                                                                               Alternative splicing. POLY-PRO.
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NEBU HUMAN

1D NEBU HUMAN

AC P2029; Q15346;
DT 10-FEB-1991 (Rel. 17, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Nebulin.

GN SUKARYOGE; Metazoa; Chordata; Craniata; Vertebra OC Eukaryote; Metazoa; Chordata; Craniata; Vertebra OC Eukaryote; Metazoa; Chordata; Craniata; Vertebra OC Mammalia; Eucheria; Primates; Catarrhini; Hominii OX NCBI_TAXID=9606;

RN H1]

RY MEDLINE=95257391; PubMed=7739042;
RA Labeit S. Kolmerer B. R.

RY MEDLINE=95257391; PubMed=7739042;
RA Labeit S. Kolmerer B. R.

RY T to muscle structure.";
RY T to muscle structure.";
RY MEDLINE=98284704; PubMed=3397062;
RN FARTIAL PRELIMINARY SEQUENCE
RX MEDLINE=88284704; PubMed=3397062;
RA BONINE B., Miranda A.F., Du J., Samitt C., Dick RA Bonilla E., Miranda A.F., Du J., Samitt C., Dick RA Bonilla E., Miranda A.F., Du J., Samitt C., Dick RA Bonilla E., Miranda A.F., Du J., Samitt C., Dick RA Bonilla E., Miranda A.F., Du J., Samit C., Dick RA Bonilla E., Miranda A.F., Du J., Samit C., Dick RA Bonilla E., Miranda A.F., Du J., Samit C., Dick RA Bonilla E., Miranda A.F., Du J., Samit C., Dick RA Bonilla E., Miranda A.F., Du J., Samit C., Dick RA Bonilla E., Miranda A.F., Du J., Samit C., Dick RA Bonilla E., Miranda A.F., Schoul B.A.;
RT "Choning and expression of human nebulin CNNAS and Granda C. Practor Compactor Compactor C. Dick RA B. Compactor 
EMBL; AF095791; AAC64968.2; -.
EMBL; AF17646; AAF68343.1; ALT_INIT.
EMBL; AF220152; AAF9557.2; -.
Genew; HGNC:11523; TACC2.
                                                                                             MIM; 605302; -. GO; GO: 0007048; P: Oncogenesis; TAS. Pfam; PF05010; TACC; 1. Coiled coil; Alter DOMAIN 43 51
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MEDLINE-98179559; PubMed=9514727;
MEDLINE-98179559; PubMed=9514727;
MEDLINE-98179559; PubMed=9514727;
MEDLINE-98179559; PubMed=9514727;
MEDLINE-98179559; PubMed=9514727;
MEDLINE-98179559; PubMed=9514727;
MEDLINE-98179; MILLOWIN STRUCTURE OF THE SH3 domain from nebulin.";
MOL. Biol. 276:189-202(1998).
MEDLINE-STRUCTURAL INTEGRITY OF SARCONGRES AND THE MENTALNING THE STRUCTURAL INTEGRITY OF SARCONGRES AND THE MENTALNING THE STRUCTURAL INTEGRITY WUSCLE-SPECIFIC. LOCATED IN THE THIN FILAMENT OF STRATED MUSCLE.

MEDLINE SPECIFICITY: MUSCLE-SPECIFIC. LOCATED IN THE THIN FILAMENT OF STRATED MUSCLE.

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R GO; GO:0030017; C:sarcomere; NAS.
R GO; GO:003792; F:regulation of actin thin filament length ac. . . .;
R GO; GO:0003792; F:regulation of actin thin filament length ac. . . .;
R GO; GO:0003707; F:sructural constituent of muscle; TAS.
R GO; GO:0007825; P:somatic muscle development; NAS.
R InterPro; IPR000900; Nebulin.
R PinterPro; IPR0018; SH3.
R PÉam; PF00018; SH3. 1.
R PENTNS; PR00510; NEBULIN.
R PRINTS; PR00510; NEBULIN.
R PROD0006; SH3; 1.
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EMBL; M19668; AAA59116.1; ALT_SEQ.
EMBL; M19669; AAA59917.1; ALT_SEQ.
PIR; S55024; S55024.
PDB; 1ARK; 28-0AN-98.
PDB; INEB; 24-DEC-97.
Genew; HGNC:7720; NEB.
MIM; 151650; -.
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us-10-031-915-36.rsp

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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      0 J. 19:4193-4203(2000).

FUNCTION: Polymerase that creates the 3' poly(A) tail of mRNA's.

Also required for the endoribonucleolytic cleavage reaction at some polyadenylylation sites. May acquire specificity through interaction with a cleavage and polyadenylation specificity factor (CPSF) at its C-terminas.

CATALYTIC ACTIVITY: N ATP + {nucleotide}(M) = N diphosphate + {nucleotide}(M+N).
                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=20402325; PubMed=10944102;
Martin G., Keller W., Doublie S.;
"Crystal structure of mammalian poly(A) polymerase in complex with an
                                                           TISSUE=Thymus;
MEDLINE=92097545; PubMed=1756732;
Wahle E., Martin G., Schiltz E., Keller W.;
"Isolation and expression of cDNA clones encoding mammalian poly(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Short;
Isold=P25500-2; Sequence=VSP 004524, VSP 004525, VSP 004526;
Isold=P25500-2; Sequence=VSP 004524, VSP 004525, VSP 004526;
Note PTM: Phosphorylated phosphorylation, dephosphorylation may regulate the interaction between PAP and CPSF.
SIMILARITY: BELONGS TO THE POLY(A) POLYMERASE FAMILY.
            Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                         MEDLINE=96221320; PubMed=8665867;
Martin G., Keller W.;
"Mutational analysis of mammalian poly(A) polymerase identifies a region for primer binding and catalytic domain, howologous to the family X polymerases, and to other nucleotidyltransferases.";
EMBO J. 15:2593-2603(1996).
                                                                                                                                                                                   TISSUE=Heart muscle;
MEDLINE=91375535; PubMed=1896071;
Mabe T., Bollum F.J., Manley J.L.;
"Prinary structure and expression of bovine poly(A) polymerase.";
Nature 353:229-234(1991).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1-20; 206-254 AND 385-396
                                                                                                                                            Wahle E.;
Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 96-102 AND 444-467,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Long;
IsoId=P25500-1; Sequence=Displayed;
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EMBL, X63436; CAA45031.1; -.
PDB, 1FSA; 13-SEP-00.
InterPro; IPR0012914; NIP transf.
InterPro; IPR001201; PAP_25A_core.
InterPro; IPR007012; PAP_cenfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                                                                                     polymerase.";
EMBO J. 10:4251-4257(1991).
                                                                                                                                                                                                                                                                                                                                                                                   19:4193-4203 (2000)
            Mammalia; Eutheria; Cel
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                "Crystal structum
analog of ATP.";
EMBO J. 19:4193-4
                              NCBI TaxID=9913
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EMBL; U52197; AAC52586.1; -.
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 274 IFPATECOKN-DIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKL 332
                                                                                                                                                                                               441 VFKKTENSENLSVDLT----YDIQSFTDTVYRQAINSKM------FEVDMKI 482
                                                                                                                                                                                                                     333 BAVDLMEPRLICVATVKRVVHRLLSIHF-----DGW-----DSEYDQWVDCESPD 377
                                                                                                                                                                                                                                 |: : : | | : | : | : | : | 483 AAMHVKRKQL------HQLLPSHVLQKKKKHSTEGVKLTPLNDSSLDLSMDSDNSM 532
                                                                                                                                                                                                                                                              378 IYPVGWCELTGYQLQ-----PPVAAEPATPLKAKEAT----KKKKKQFGKKRK 421
                                                                                                                                                                                                                                                                             593 SIPQTATQPAISSPPKPTVSRVVSSTRLVNPPPRPSGNAAAKIPN---PIVGVKRTSSPH 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Polymerase that creates the 3' poly(A) tail of mRNA's. Also required for the endoribonucleolytic cleavage reaction at some polyadenylylation sites. May acquire specificity through interaction with a cleavage and polyadenylation specificity factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=96189120; PubMed=8628305;
Zhao W., Manley J.L.;
"Complex alternative RNA processing generates an unexpected diversity
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kashiwabara S., Noguchi J., Zhuang T., Ohmura K., Honda A., Sugiura S., Miyamoto K., Takahashi S., Inoue K., Ogura A., Baba T.; "Regulation of spermatogenesis by testis-specific, cytoplasmic poly(A) polymerase TRAP.' Science 298:1999-2002(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                      PAP MOUSE STANDARD, PRT; 738 AA. Q61208; Q61208; Q61209; Q8K4X2; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last sequence update) PolyMerase alpha (EC 2.7.7.19) (PAP) (Polymucleotide adenylyltransferase). PAPOCA OR PAP OR PLAP. Mus musculus (Mouse).
                                                                                                                                  3.7%; Score 98.5; DB 1; Length 738; llarity 20.9%; Pred. No. 2.5; Conservative 33; Mismatches 105; Indels 6:
                                                                                                               82310 MW; DOB90662F89363E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
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1. Cell. Biol. 16:2378-2386(1996)
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MEDLINE=22359775; Pubmed=12471261;
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                                                                                                                                                                                                                                                                                                                                                 482 LPVSVENIKOETDD 495
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                                                                                                    493
738 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            Name=3; Synonyms=V;
IsoId=Q61183-3; Sequence=VSP_004529, VSP_004530;
Name=4; Synonyms=V1;
IsoId=Q61183-4; Sequence=VSP_004527, VSP_004528;
PTM: Phosphorylated. Phosphorylation/dephosphorylation may regulate the interaction between PAP and CPSF (By similarity).
SIMILARITY: BELONGS TO THE POLY(A) POLYMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRNA processing; Transferage; Transcription, RNA-binding;
BNDsphorylation; Nuclear protein; Alternative splicing.
INIT MET 112 112 BY SIMILARITY.
ACT SITE 114 114 BY SIMILARITY.
ACT SITE 166 BY SIMILARITY.
VARSPLIC 279 292 EWPNPVLIKQPEEC -> YVFRLYYNKIDCRH (in
(CPSF) at its C-terminus (By similarity).
CATALYTIC ACTIVITY: N ATP + {nucleotide}(M) = N diphosphate {nucleotide}(M+N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPSDRYHLMPIIT -> SVLFFPLQIHTIQ (in
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Missing (in isoform 3).
/Frid-vSP 004530.
|Frid-vSP 004531.
                                                                                                                                                                                                                                                                Name=2; Synonyms=III;
IsoId=261183-2; Sequence=VSP_004531, VSP_004532;
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                                                                                        -1- SUBUNIT: Monomer (By similarity).
-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
-1'- ALTERNATUE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
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AB086644; BAC00996.1; JOINED.
AB086645; BAC00996.1; JOINED.
AB086647; BAC00996.1; JOINED.
AB086647; BAC00996.1; JOINED.
AB086649; BAC00996.1; JOINED.
AB086649; BAC00996.1; JOINED.
PE5500; 175A.
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InterPro; IPR002934; NTP_transf.
InterPro; IPR001201; PAP_25A core.
InterPro; IPR007012; PAP_centr.
InterPro; IPR007010; PAP_RNA_bind.
Pfam; PP04926; PAP_RNA-bind; I.
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                            274 IFPATFCORN-DIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNWDCPNHGFKVGMKL 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 IYPVGWCELTGYQLQ------PPVAAEPATPLKAKEAT----KKKKKQFGKKRK 421
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QUUBW7; 043212; 043434; 060898; Q9H538; Q9UEU2;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annota
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Reiter A., Sohal J., Kulkarni S., Chase A., Macdonald D.H.C.,
Aguiar R.C.T., Goncalves C., Hernandez J.M., Jennings B.A.,
Goldman J.M., Cross N.C.P.;
"Consistent fusion of ZNP198 to the fibroblast growth factor receptor-
1 in the t(8.13) (p11,q12) myeloproliferative syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVPSPTSAMKTSPLNSSGSSQGRNSPAPAVTAASVTSIQASEVSVPQANSSESPGGPSSE
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MEDILINE-291079818, PubMed=9889006;
MEDATATI S., Reiter A.J., Smedley D., Goldman J.M., Cross N.C.P.;
"The genomic structure of ZNF198 and location of breakpoints in the t(8;13) myeloproliferative syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98245146; PubMed=9576949;
Popovici C., Adelaide J., Ollendorff V., Chaffanet M., Guasch G., Jaczot M., Leroux D., Birnbaum D., Pebusque M.-J.,
Fibroblast growth factor receptor I is fused to FIM in stem-cell myeloproliferative disorder with t(8:13) (pi2;q12).";
Proc. Natl. Acad. Sci. U.S.A. 95:5712-5717(1998).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           69;
                                                                                                                                             3.7%; Score 98.5; DB 1; Length 738; 21.4%; Pred. No. 2.5;
                                                                                                                                                                                                        Indels
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Blakey S., Wall M.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
[5]
                           /FTId=VSP 004532.
K -> L (IN REF. 1):
168E8757143EF1F6 CRC64;
   Missing (in isoform 2).
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                                                                                                                                                                                                        34; Mismatches
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82177 MW;
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738
                                                          46
738 AA;
                                                                                                                                                                         Similarity
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375
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REDINE-98085877; PubMed=9425908;

Xiao S., Nalabolu S.R., Astra J.C., Ma J., Abruzzo L., Jaffe E.S.,
A Xiao S., Nalabolu S.R., Astra J.C., Ma J., Abruzzo L., Jaffe E.S.,
Ry Stone R., Weissman S.M., Hudson T.J., Fletcher J.A.;
Ry T. "FGFR1 is fused with a novel zinc-finger gene, ZNF198, in the t(8;13)
RT "FGFR1 is fused with a novel zinc-finger gene, ZNF198, in the t(8;13)
RT leukemia/lymphoma syndrome.";
RI leukemia/lymphoma syndrome.";
RL OFFICION: May function as a transcription factor.
CC -- FUNCTION: May function as a transcription factor.
-- FUNCTION: May function as a transcription factor.
-- SUBCELLULAR LOCATION: Nolear (Potential).
CC -- SUBCELLULAR LOCATION: Nolear (Potential).
CC -- SIMILARITY: Contains S NTM-type zinc fingers.
CC -- SAMILARITY: Contains S NTM-type zinc fingers.
CC -- CAUTION: Ref. S sequence differs from that shown due to a frameshift in position 330.
CC -- CAUTION: Ref. S sequence differs from that shown due to frameshifts
CC -- CAUTION: Ref. S sequence differs from that shown due to frameshifts
CC -- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWN="http://www.infobiogen.ff/services/chromcancer/Genes/ZNF198ID114.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its mochant in inno way modified and this statement is no removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE OF 152-1377 FROM N.A.
MEDLINE=98361795; PubMed=9694728;
Still I.H., Cowell J.K.;
"The L(8;13) atypical myeloproliferative disorder: further analysis of the ZNF198 gene and lack of evidence for multiple genes disrupted on chromosome 13.";
                                                                                                                                                                                                                                                                                                                                                                                                           Warren W., Abdul-Rauf M., Somers
                                                                                                                                                                                                                                                                                                                                                                                               Smedley D., Hamoudi R., Clark J., Warren W., Abdul-Rauf M., Somers Venter D., Fagan K., Cooper C., Shipley J.;
"The t(8,13) (p11,q11-12) rearrangement associated with an atypical myeloproliferative disorder fuses the fibroblast growth factor receptor 1 gene to avvel gene RAMP.";
Hum. Mol. Genet. 7:637-642 (1998).
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MEDLINE=98167848; PubMed=9499416;
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"Isolation and characterization of two homologous cDNA clones from
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(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
             Torpedo electromotor neurons.";
DNA 8:555-561(1989).
                                                                                                                                                                                                                  EMBL, M30270; AAA49279.1; -. PIR; A33319; A33319.
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nes 74; Conservative
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721 AA;
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ID_CBFS_CANAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 NHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHFDG-WDSEYDQWVDCESPDIYPV 381
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                                                                                                                                                                      -> GWLKWIQV
                                                                                                                                                                                                                                                                                                                                                    157 WCHMWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGG
                                                                                                                                                                                                                                                                                                                                                                                                      217 WFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLM----ICVDGGPSTDGLDW-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                745 ------VVRDFČSEDCCKKFQDWYYKAARCDCCKSQGTLKERVQWRGEMKHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----MKNKAV-LCKPLTMTKATYCKPHMQTKSCQTDDTWRTBYVP-VPIPVPVYIPV
                           MIM; 602221; -.
GO; GO:0008270; F:zinc ion binding activity; NAS.
Transcription regulation; Nuclear protein; Chromosomal translocation;
Repeat; Zinc-finger...
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Electromoctor neuron-associated protein 1 (Fragment).
Torpedo californica (Pacific electric ray).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes, Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
                                                                          MYM-TYPE 1 (POTENTIAL).
MYM-TYPE 2 (POTENTIAL).
MYM-TYPE 3 (POTENTIAL).
MYM-TYPE 4 (POTENTIAL).
MYM-TYPE 5 (POTENTIAL).
MYM-TYPE 5 (POTENTIAL).
MYM-TYPE 5 (POTENTIAL).
ZNETSPEPTIAL).
                                                                                                                                                               VACUDESSERVETCSTSCLELYEDKONPT -> GW
SPSRNSVVTSCLISLMKNNRILL (IN REF. 1)
NW -> ASL (IN REF. 4).
K -> G (IN REF. 1).
MISSING (IN REF. 4).
MISSING (IN REF. 6).
DF -> IS (IN REF. 6).
DF SIGNO (IN REF. 6).
MISSING (IN REF. 6).
MW; 2652D4C766492FF9 CRC64;
                                                                                                                                                                                                                                                                                               3.6%; Score 96.5; DB 1; Length 1377;
20.2%; Pred. No. 8.4;
iive 46; Mismatches 147; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, E
Torpediniformes, Torpedinoidei, Torpedinidae, Torpedo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PMHMYSQNIPVPTTVPVPVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90091742; Pubmed=2480872;
Ngsee J.K., Scheller R.H.;
                                                                                                                                                                                                                                             1009 1010
1016 1016
1377 AA; 154910 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: :: | |
993 SSMPDVPYEPD 1003
             Genew, HGNC:12989; ZNF198
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 20.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 VSVENIKQETD 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                      416
                                                                                                                                                                                                                                  967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7787;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442
                                                                 Repeat; Z
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
SN_FING
                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 ------NKAKTGLILDNGKDAEISF---PYLTSISSLIVWHPANPSEKIVRALFPGNA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 PNHGFKVGM-KLEAVDLMEPRLI------CVATVKRVVHRLLSIHFDGWDSEXDQWV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604 RPRTELQSKPEEKDAKAKADAAKQELEEKMOKDEKLKSESKPKPLKEKIVKKEVKAKKPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 LINKLCVKPEPLFRTVGNVIDPVILFQKMGVGRLEMYILNSVKGSKE---LQFFMQHWSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 AIFPATFCOKNDIELTPPKGYEAQ-TFNWENYLEKTKS-----KAAPSR-----LFNMDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 D----CESPDIYPVGWCELIGYQLQPPVAAEPATPLKAKEATKKKKKQFGKKRKRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 LGNICV-----ATVCKVL------LDGYLMICVDGGPSTDGLDWFCYHASSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                          ORGANELLES.
-1- MISCELLARDOUS: HAS A HIGHLY BASIC REGION WITH MANY COPIES OF THE SEQUENCE KKE, REPEATED BUT NOT AT FIXED INTERVALS.
-1- SIMILARITY: TO ELECTROMOTOR NEURON-ASSOCIATED FROTEIN 2.
-!- SUBCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES OF INTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 ------PPTKTRPLRQGSKKPLLEDDPQGARKISSE----PVPGEIIAVRV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6%; Score 95.5; DB 1; Length 721; 22.2%; Pred. No. 4.3; .ve 45; Mismatches 112; Indels 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 X 3 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721
81241 MW; B53E69A9F309CE00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLU/LYS-RICH (BASIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 -- KEEHLDV----ASPDKASSPELPVSVENIKOE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          664 EKKREEKDVKKESAKPDRKEEKAV-IKXEKVKK3 696
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Fri Feb

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343 ERDTYPRRWGLGPIAQKKKQMKADGKLDKYGR-VNENTPENWKKDYKDL-DEQPAPPIPE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILARITY: Belongs to peptidase family M12B.
-:- SIMILARITY: Contains I disintegrin-like domain.
-:- SIMILARITY: Contains I PLAC domain.
-:- SIMILARITY: Contains 8 TSP type-1 domains.
                                                                                                                                                                                                                                                                PRT; 1593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002870; Pep_M12B_propep
IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Petal lung;
MEDLINE=21264577; PubMed=11279086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR006025; Zn MTpeptdse.
fam; PF01562; Pep_M12B_propep; 1.
fam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ250725; CAC20419.1;
Genew; HGNC:14605; ADAMTS12.
                                                                                                                     438 PLLEDDPQGARK 449
                                                                                                                                                            461 RKAEDDSSKSEK 472
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 606184; -.
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                                                                                                                                                                                                                                                                AT12 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ESLLVGYKRVVV----KDSAVNSVCYGAK--LMIPGLLRYEEGIEL-----YD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 AQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGM-KLEAVDLMEPRLICVATVKR--- 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFBEGMKLEAIDPLNLGN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EVVLMTTKGEA------IAIGIAQMSTVDLQSCDHGIVAKVKRCIM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPP--- 394
Centromere/microtubule binding protein CBF5 (Centromere-binding factor
5) (Nucleolar protein CBF5).
                                                                                                                                                                                                                                                                BE IN
                                                                                                                                                                                                                       IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 ATRLVKS-----QQGAGKEYVCIVRLHEQLKDDKELNR----ALENLTGALFQRPPLISA
                                                                                                                                                                                                                                                                                                         SIMILARITY).
SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
SIMILARITY: Contains 1 PUA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 NDASHDFWCNLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPSSHEV------VAWI---KRILRVEKTGHS-----GTLDPKVTGCLIVCIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 HIKMVESMKYPFRQGMRLEVV------DKSQVSRTRMAVVDTVIGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----REVELLYEDGDSDDD-----FWC-----HMWSPLIH----PVGWS----RRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 173; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U59149; AAB84297.1; -

R InterPro; IPR004802; Cbf5.

R InterPro; IPR0042478; PUA.

R InterPro; IPR0042278; PUA.

R InterPro; IPR004221; Unchar_dom_2.

R InterPro; IPR004221; Unchar_dom_2.

R Pfam; PP01472; PUA; 1.

R SMART; SM00359; PUA; 1.

R TIGRFAMS; TIGR00425; CBF5; 1.

R TIGRFAMS; TIGR00451; unchar_dom_2; 1.

R PROSTITE; PS50890; PUA; 1.

M Microtubules; Centromere; Repeat; Nuclear protein; DNA-binding.

DOMAIN 267 342
                                                                                                                                                                        Jiang W., Clifford J., Koltin Y.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS IN VITRO TO CENTROMERES AND MICROTUBLES. IT I
CENTROMERE DNA-CEP3-BINDING FACTOR AND IS INVOLVED IN MITOTIC
CHROMOSOME SEGREGATION. IT IS ESSENTIAL FOR CELL GROWTH. MAY B
SOME MAY ASSOCIATED WITH THE CBF3 110 KDA SUBUNIT (CBF3A) (BY
                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 AA; 54321 MW; 3BAF5104E12C9EB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.4%; Score 92.5; Di 20.9%; Pred. No. 4.4;
                                                         Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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8 ద ò 셤 Š B ઠ 원 ઠે B. ò 셤

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437
                                                                                 401 SKLVAPEPOLPKKKSLIEEVEVDIDVEDKSEKKEKKDKKEKKEKKDKKEKKEKKEKKOKKEKK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADATS-12 precursor (BC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-TS12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARLITO.
SINDIAGRITO.
SINDIAGRITO.
SINDIAGRITO.
SINDIAGRITO.
SUBJECTED TO AN INTRACELLULAR MATURATION PROCESS LEADIND.
TO A FRAGENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALLOPROTEINASE, DISINTEGRIN-LIKE, CYS-RIGH AND TS-1 DOMAINS AND
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR TS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMÁIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VAAEPATPLKA-----KEATKKKKKOFGKKRKRIPPTKTRPLRQGSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matrix (By similarity).
-!- TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is wic expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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HASSHAIFPATFCOKN----DIELTPPKGYEAQTFNWE---NYLEKTKSKAAPSRLFNM
                                                                      DGSSCQTVRKMFKQKEGSGYVDIGLIPKGARDIRVMEIEGAGNFLAIRSED--PEKYY--
                                                                                                                                   --LNGGFIIQWNGNYKLAGTVFQYDRKGDLEKLMATGPTNESVWIQLLFQVTNPGIKYEY
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                                                                                                                                                                                                                                                                                                                                                                         Zea mays (Maize).
Zea mays (Maize).
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. W22;
MEDLINE=91227140; PubMed=1709276;
MEDLINE=91227140; PubMed=1709276;
MEDLINE=91227140; PubMed=1709276;
Macafimahatratra P., Chaubet N., Philipps G., Gigot C.;
"Nucleotide sequence and expression of a maize H1 histone cDNA.";
Nucleic Acids Res. 19:1491-1496(1991).
-!- FUNCTION: HISTORES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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                                                                                                         DCPNHGFKV----GMKLEAVDL-----MEPRLICVATVKRVVHRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D1FD73DAA74A6778 CRC64;
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ARG/LYS-RICH (BASIC).
GLOBULAR.
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1 INIT MET

1 OMAIN

31 ASP/GLU-RICH (ACIDIC)

POMAIN

31 45 ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1.
                                                                                                                                                                                                                                                                               245
                                                                                                                                                                                                   811 TİQKDĞLDNDVEQMYFWQYGHWTEC 835
                                                                                                                                                                      SIHFDGWDS-----EYDQWVDC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005819; Histone H1/H5.
InterPro; IPR005819; Histone H5.
InterPro; IPR003216; Linkerhist N.
Pfan; PF00538; linker histone; I.
PRINTS; PR00624; HISTONEHS.
ProDom; PD000373; Linkerhist N; 1.
SWART; SM00526; H15; 1.
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PIR; S26826; S26826.
MaizeDB; 25540; -.
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18.4%; Pred. No. 22;
[ve 59; Mismatches 166; Indels 187; Gaps
          PROSITE; PSS015; ADAM MEPRO; 1.
PROSITE; PS0046; CYSTEINE SWITCH; FALSE NEG.
PROSITE; PS00546; CYSTEINE SWITCH; FALSE NEG.
PROSITE; PS0014; DISINTEGRIN_2; FALSE_NEG.
PROSITE; PS50092; TSP1; 6.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen; Repeat; Extracellular matrix.
POTENTIAL.

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ADAMTS-12.
METALLOPROTEASE.
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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SEQUENCE STRAIN=S286C / AB972;

MEDINTE-97313271; PubMed=9169875;

Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A Chung E., Churcher C.M., Coster F., Davis R.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,

Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

A Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D.,

Mueller-Auer S., Namath A., Nenralle D., Schaffer M., Scharfe M.,

Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,

Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

A Zhong W.W., Zollner A., Vo D.H., Hani J.;

Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0000123; C:histone acetyltransferase complex; IDA.
GO; GO:0004402; F:histone acetyltransferase activity; IDA.
GO; GO:0016573; P:histone acetylation; IDA.
GO; GO:0016357; P:regulation of transcription from Pol II pro. . ; IMP.
InterPro; IPR000953; Chromo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11036083;
Eisen A., Utley'R.T., Nourani A., Allard S., Schmidt P., Lane W.S.,
Lucchesi J.C., Cote J.;
Subunits important for transcriptional regulation.";
J. Biol. Chem. 276:3483-3491(2000).
-i- FUNCTION: MAY PLAY A ROLE IN TRANSCRIPTION REGULATION AS PART OF
THE NUA4 COMPLEX.
-i- SUBUNIT: COMPONENT OF THE NUA4 HISTONE ACETYLTRANSFERASE COMPLEX.
                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
(Rel. 39, Last sequence update) (Rel. 41, Last annotation update)
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                                                                                                                           401 AA.
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                                                                                                                           PRT;
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30-MAY-2000 (Rel. 39, Last seq
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EAF3 OR YPR023C OR YP9367.03C
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SMBL; Z49274; CAA89277.1; -.
PIR; S54497; S54497.
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290 PKGYEAQTFN-WENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLI--CVA 346
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                                                                                                     Gaps
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                                                                      Length 401;
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SMART; SM00298; CHROMO; 1.
Transcription regulation; Nuclear protein.
SEQUENCE 401 AA; 45203 MW; 63758DE9510D70DC CRC64;
                                                                                                     58;
                                                                    3.4%; Score 91; DB 1;
23.0%; Pred. No. 4.7;
ative 29; Mismatches 58
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1 MKGMKVEVLNSDAVLPSRVY......KASSPELPVSVENIKQETDD 495
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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SUMMARIES			Π	AAM39576	AABG0488	AAM41362	ABB05680	ABB89448	AAY79183	ABU03557	ABB78695	ABB70683
			DB	22	2	22	23	23	21	24	23	22
			Score Match Length DB I	495	495	448	617	329	631	410	410	891
	%	Query	Match	100.0	100.0	8.06	81.4	62.9	52.6	52.0	51.7	41.4
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ALIGNMENTS

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Human, nootropic, immunosuppressant, cytostatic, gene therapy, cancer, peripheral nervous system, neuropathy, central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease, haemostatic, amyotrophic lateral sclerosis; Shy-Drager Syndrome, chemotactic, chemokinetic, thrombolytic; drug screening; arthritis; inflammation;
                    AAM39576 standard; Protein; 495 AA.
                                                                                         Human polypeptide SEQ ID NO 2721.
                                                                                                                                                                                                                                                                                                                                      2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                  26'-DEC-2000; 2000WO-US34263
                                                                   (first entry)
                                                                                                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                        21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000;
                                                                                                                                                                                                                                            26-JUL-2001.
                                                                                                                                                                                                                                                                                                    15-APR-2000;
                                                                   22-OCT-2001
                                                                                                                                                                          leukaemia.
                                            AAM39576;
RESULT 1
            AAM39576
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                                                                                               immunosuppressant and cytostatic activity. The polymucleorides are useful in gene therapy. A composition containing a polymeptide or polymucleotide of the invention may be used to track as of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activithibin activity, chemoteatic/chemokinetic activity, demonstration and thrombolytic activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWCAINSKILVPPRTIHAKFTDWKGYLAKRLVGSRTLPVDFHIKMYBSWKYPPRQGMRLE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKVLLDGYLMI CVDGGFSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed
                                                               Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKGMKVEVILNSDAVI.PSRVYMIASVIQTAGYRVILLRYEGFENDASHDFWCNLGTVDVHPI
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                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                              Ren F, W
Zhang J;
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                                                              Qian XB,
Yang Y,
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100.0%; Pred. No. 1.5e-269;
ive 0; Mismatches 0;
                                                            Chen R, Ma Y, (
Xu C, Xue AJ,
t, Drmanac RT;
                                                                                                                                                                                                                                  Example 4; SEQ ID NO 2721; 10078pp; English.
                                                               Chen R,
                                                              Asundi V, Che
Wehrman T, Xu
Goodrich R,
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29-NOV-2000; 2000US-0727344
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                                                              Liu C, A
Wang Z, W
Zhou P,
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495, Conserv
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                               (HYSE-) HYSEQ INC
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C.N.S disorders
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Corpus AAB60453-AAB60506 represent 54 human cell cycle and proliferation proteins (CCYPR), which are encoded by AAF59590-AAF59643. CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with coveragnession of functional CCYPR, Monoclonal or Dolyclonal antibodies to CCYPR may be used in enzyme-linked immunosobatt assays (ELISA) or radioimmunoasays to detect CCYPR. CCYPR itself may be used to detect compounds e.g., antibodies, oligonuclectides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that modulate the activity of CCYPR. CCYPR nucleotides can be used to generate transgenic animal models of human collectides can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR. Treatment or prevention of a disorder associated with CCYPR. Diseases which can be diagnosed, treated and prevented using CCYPR proteins, nucleic acids, agonists or antegonists include immune, developmental and cell signalling disorders, and cell proliferative disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allergies, diabetes mellitus, disorders of the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                                                                                                                                                                                                          Human cell cycle and proliferation protein CCYPR-36, SEQ ID NO:36
                                                                                                                                                                                                                                                                                                                                                                                                                                       cell cycle and proliferation protein; CCYPR; human; agonist; antagonist; gene therapy; detection; gene therapy; transgenic animal disease model; immune disorder; developmental disorder, cell signalling disorder; cell proliferative disorder; cancer; tumour; anaemia; epilepsy; arteriosclerosis; asthma; allergy; diabetes mellitus; menstrual cycle disorder; bacterial infection.
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Baughn MR, Patterson C, Shah
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                                                                                                                                                                            AAB60488 standard; Protein; 495
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Lu DAM,
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99US-0153129.
99US-0164647.
481 ELPVSVENIKQETDD 495
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N-PSDB; AAF59625.
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Y, Yang J,
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(HYSE-) HYSEQ INC
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                                                                                                                                                                                      61 GWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE
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                                                                                                     1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
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                          Gape
                        Indels
ilarity 100.0%; Pred. No. 1.5e-269; Conservative 0; Mismatches 0;
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2000US-0653450.
2000US-0662191.
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  Local Similarity
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25-APR-2000;
09-JUL-2000;
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 FWCNLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVE 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed specification.
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   Ren F, W
Zhang J;
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   Qian XB,
Yang Y,
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99.8%; Pred. No. 6.1e-244;
iive 0; Mismatches 1;
Chen R, Ma Y, C
Xu C, Xue AJ,
l, Drmanac RT;
                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 6293; 10078pp; English.
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      Chen R,
Asundi V, Che
Wehrman T, Xu
, Goodrich R,
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N-PSDB; AAI60518.
Liu C, A
Wang Z, W
Zhou P,
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Best Local Similarity
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511 ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF 570
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                                                                                                                                                                                                 (first entry)
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N-PSDB; ABL89857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes assemblages and computer readable media comprising novel human cDNA sequences and clones derived from human foetal brain, foetal kidney, melanoma, testis and amygdala cDNA libraries. ABA93702 to ABA93766 represent human cDNA sequences from the present invention which encode the proteins given in ABB05662 to ABB05729. The human cDNA sequences and clones can be used in gene therapy. The clones may be used in a variety of applications, for example they may be used in profilling assays, for providing large arrays of human genetic material for implementing large-scale screening strategies and for treating diseases via gene therapy procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERRSDWAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKGMKVEVINSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA sequences and clones derived from human fetal brain, kidney, melanoma, testis and amygdala cDNA libraries, useful in screening and therapy -
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                                                                                                                     Human; foetal brain; foetal kidney; melanoma; testis; amygdala; gene therapy; chromosome 22q13.31-13.33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 1.2e-217;
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0
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100.0%; Pred. No. 1...
0; Mismatches
                                                                                               Human transmembrane protein clone amy2_li14.
                                                                                                                                                                                                                                                                                                                      (GEHU-) GERMAN HUMAN GENOME PROJECT.
       ABB05680 standard; Protein; 617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 130; 611pp; English.
                                                                                                                                                                                                                                                             25-APR-2001; 2001WO-IB02050.
                                                                                                                                                                                                                                                                                         25-APR-2000; 2000US-199380P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
es 397; Conservative
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-055860/07.
N-PSDB; ABA93718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    617 AA;
                                                                                                                                                                                                  WO200198454-A2.
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                               27-DEC-2001
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The invention relates to novel genes (AB189449-AB190853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointeetinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chamelytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epizatic infections diseases such as wiral, bacterial, fungal and parasitic infections diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antifulgal; antiulcer; vulnerary; anticonvulsant; antidacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 11; SEQ ID NO 1824; 2081pp + Sequence Listing; English.
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                                                                                              571 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAA
361 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAA
                                                                                                                                                                                                                                                                                                                                                               ABB89448 standard; Protein; 329 AA.
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16; Gaps

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241 CKVILDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
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                                                                                                                                                                                                                                                                                                                                                                              2 KGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDKSQVSRTRMAVVDTVIGGRIRLLYBDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDITKKODGH -----FDTPPHLFAKVKEVDQSGEWFKEGMKLEAIDPLNLSTICVATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 ENYLEKTKSKAAPSRIFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF
transcription factors, splicing factors, capping factors, transport proteins, translation factors or replication factors that modulate HSC activity, especially differentiation or replication. The invention provides claimed methods: for identifying PHSC-specific nucleic acids; for generating a stem cell/progenitor cell from PHSCs; for identifying the presence of a PHSC in a sample; for identifying the presence of a PHSC in a sample; for identifying the presence of a compound that modulates HSC activity; for using such a compound to treat an immune system acid into a HSC; and for ex vivo expansion of HSCs. Also claimed are vectors, host cells, and an antibody that specifically binds a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKRIPPIKIRPLROGSKKPLLEDDPQGARKISSEPVPGELIAVRVKEE 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis-associated human protein sequence #102
                                                                                                                                                                                                                                                                                            52.6%; Score 1410; DB 21;
56.2%; Pred. No. 4.6e-137;
iive 67; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 410 AA.
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 56.2<sup>†</sup>
Matches 263; Conservative
                                                                                                                                                                                                                     an HSC-specific protein.
                                                                                                                                                                                                                                                               631 AA
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  61 GWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE
                                                                                                                                                                                                                                                181 SERRXDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMXLEAIDPLNLGNICVATV
                                                                                                                                            121 VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM
                                                                                                                                                                     181 SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
                                                                                                                                                                                                                                                                                                     CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hematopoietic stem cell signaling proteins modulating replication and differentiation for treating immune system disorders and leukaemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haematopoietic stem cell; immune system disorder; leukaemia; antileukaemic; immunomodulator; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haematopoietic stem cell specific protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY79183 standard; Protein; 631 AA
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ABB78695 standard; Protein; 410

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RESULT 8
ABB78695
                                                                                                                                                                                                                                                                                                                                                                                                      detecting an angiogenesis-associated transcript in a cell in the pustent with a method involves contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence at least 80 identical to any of the angiogenesis-associated human polymucleotide sequences given in the specification. These angiogenesis-associated polymucleotide sequences comprise genes that exhibit changes in expression levels as a function of time in tissue undergoing angiogenesis. The method and the polymucleotide sequences of the invention are useful for diagnosing and treating angiogenesis and angiogenesis-associated diseases e.g. cancer. The polymucleotide sequences are also useful in the gene therapy of such disorders. The angiogenesis-associated proteins encoded by the polymucleotide sequences are useful as a vaccine for therapeutic and prophylactic immunisation. Abu03456-ABU03569 represent angiogenesis-associated immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 WGAASGKPLVPPRIIQHXYINWKAFLVKRLIGAKTLPPDFSQKVSESMQYPFKPCMRVEV 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 RKVLADGFLMIGIDGSEAADGSDWFCYHATSPSIFPVGFCEINMIELTPPRGYTKLPFKW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 ENVRVEVPNTDCSLPTKVFWIAGIVKLAGYNALLRYEGFENDSGLDFWCNICGSDIHPVG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 VDKRHLCRTRVAVVESVIGGRLRLVYEESEDRTDDFWCHMISPLIHHIGWSRSIGHRFKR
                                                                                                                                                                                                                                                           Detecting angiogenesis-associated transcript in a cell for diagnosing and treating cancer by contacting a sample with a polynucleotide that exhibits changes in expression level as a function of time in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLEV
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                                                                                                                                                                                                                                                                                                                                                                                            invention relates to methods and compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aziz N;
                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 275; 291pp; English.
                                                                                                                                                                   Watson SR,
                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
               2001US-0791390.
2001US-285475P.
2001US-310025P.
2001US-350666P.
                                                                   13-NOV-2001; 2001US-350666P.
29-NOV-2001; 2001US-334244P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249; Conservative
                                                                                                                                                                                                                                                                                                                     undergoing angiogenesis
                                                                                                                                                                   Glynne R,
                                                                                                                                                                                                       WPI; 2003-040681/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein sequences
                                                                                                                                                                                                                         N-PSDB; ABX08841.
14-FEB-2001;
22-FEB-2001;
                                                     03-AUG-2001;
                                   19-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                              present
                                                                                                                                                                   Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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The present invention describes a substantially pure nematode C. elegans (Caenorhabditis elegans) nucleic acid (I) encoding a LIN-8 polypeptide (see ABB78648), or LIN-6 polypeptide (see ABB78648), or LIN-6 polypeptide (see ABB78650), where the polypeptides comprise at least 130, 110, 130 contiguous amino acids of the 386, 322 and 498 amino acid sequences given in ABB78648 to ABB78650, and modulate cell proliferation. (I) has contiguous acity of a cell, and for identifying the compound that modulates cell proliferation. (I) is useful for modulates cell proliferation. (I) is useful for modulates cell proliferation (I) can be used for identifying the compound that modulates call proliferation. (I) as useful for the presence of the cell proliferation disease, or an increased chance of developing the disease, by measuring lin-8, Lin-56 or Lin-61 proliferation disease, or an increased chance of developing the disease, by measuring lin-8, Lin-56 or Lin-61 proliferation disease.

(I) is also useful for identifying the compound that modulates cell using Ab or measuring amount of lin-8, lin-56, lin-61 mRNA in the sample.

(I) is also useful for identifying the compound that modulates cell proliferative diseases including cancer, as well as in diagnosing and treating cell proliferative diseases. (I) is also useful for identifying the compound that modulates condentifying the compound that modulates cell proliferative diseases such as mammals and may be used to identify therapeutic compounds. The present sequence represents a human has (heat shock protein) brotein which is given in comparison with the comparison with the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 WCAINSKILVPPRIIHAKFIDWKGYLMKRLVGSRILPVDFHIKMVESMKYPFRQGMRLEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Caenorhabditis elegans nucleic acid involved in tumor suppressor pathway, encoding LIN-8, LIN-56 or LIN-61 polypeptide, useful for diagnosing and treating cell proliferative diseases such as cancer
                                                                                                                                                                  Caenorhabditis elegans; lin-8; lin-56; lin-61; tumour suppressor; cell proliferation; nematode; cancer; mutant.
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62.6%; Pred. No. 5.7e-135;
.ive 56; Mismatches 84;
                                                                                                                             Human hap BAA90919 protein sequence SEQ ID NO:68
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 8; 116pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2000; 2000US-208802P
                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001; 2001WO-US17909
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248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horvitz HR, Davison EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-401590/43.
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                                                                                 17-JUL-2002
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                           13-DEC-2001
                                         ABB78695;
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S
                                                                                                                      SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 240
                                                                                                                                                          CKVILDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIBLTPPKGYBAQTFNW 300
                                                                                                                                                                                                                                                                                                                                                                 301 ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF 360
VDKSQVSRTRMAVVDTVIGGRLRLLYEDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                   Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGWEEEYDQWVDCESPDLYPVGWCQLTGYQLQPPAS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
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N-PSDB; ABL14786.
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Length 891;

DB 22;

41.4%; Score 1111;

Query Match

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14;
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                                                                                                                                                    115 QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRV 174
                                                                                                                                                                                                                                                            221 GMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATF 279
                                                                                                                                                                                                                                                                                                                  280 CQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLME 339
                                                                                                                                                                                                                                                                                                                                              568
                                                                                                                                                                                                                                                                                                                                                                        394
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                                                                                                                                                                                                                                                                                                                                                                                                                            -VAAEPATFLKAKEATKKKKKQFGKKRRIPPTKTRPLRQGSKKPLLEDDPQGARKISSE 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 PVPGEIIAVRVKEEHLDVA----SPDKASSPELP-----VSVENIKQETDD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                              55 VDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFR
                                                                                                                                                                                                                                                                                                                                  277 AEVHSVGWCATRGKPLIPPRTIEHKYKDWKDFLVGRLSGARTLPSNFYNKINDSLQSRFR
                                                                                                                                                                                                        GHGI------KWSERRSDMAHHPTFRKIYCDAVPYLFK---KVRAVYTEG--GWFEE
                                                                                                                                                                                                                                                                            3 GMKVEVLNSD----AVLPSRV---YWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      629 QQAPKPAPKPKIQRKRKPKKGAAGGK----TPTDNNTQSVKSRTIALKTTPH-----
               Gaps
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              6.8;
              Indels
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43.4%; Pred. No. 9.4e-106; ative 75; Mismatches 162;
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11-JUL-2000; 2000US-0614150.
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             234; Conservative
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Best Local Similarity
Matches 234; Conserv
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rebroprotective; cytostatic; rheumatic; gene therapy;
                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL30511), and the encoded proteins
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                     ID NO 27069; 21pp + Sequence Listing; English
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                                                                                                                                                                                                 Query Match
41.4%; Score 1111; DB 22;
Best Local Similarity 43.4%; Pred. No. 1.6e-105;
Matches 234; Conservative 75; Mismatches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTB). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolyysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDF--WCHMWSPLIHPVGWSRRVGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 WCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYP---FRQGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 GIXMSERRSDMAHHPTFRKIYC-----DAVP-YLF--KKVRAVYTEGGWFEEGMKLEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
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                                                                                                                                                                                                                                                                                               Zhang J,
RT;
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Drmanac 1
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Wehrman T,
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                                                                                                                                                                                             11-SEP-2000; 2000US-0659671
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Yang Y,
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Homo Bapiens.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; noctropic; neuroprotective; antiparkinsonian; artidiabetic; immunosuppressive; dermaclogical; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
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k, Wang Z, 'Ghosh M;
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na Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
465 KEEHLDVASP--DKASSPELPVSV 486
                                          506 YFNHRCFSGPYLNKGRIABLPQCV
                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 1614.
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J. Wang D,
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Yang Y, Ma
T, Wang J,
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Wehrman T,
                                                                                                                                                                                                                                                                              ABP69567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                    RESULT 12
                                                                                                                                                                                  ABP69567

ABP69567

ABP69567

ABP6

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15;

Gaps

99

Indels

Length 894;

22.8%; Score 611; DB 23; 34.1%; Pred. No. 8.8e-54; ive 65; Mismatches 170;

Conservative

Query Match Best Local Similarity Matches 156; Conserv

Sequence

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298
                                                                                                                                                                                                                                                       333
                                                                                                                                                                                                                                                                                                               356 ILPVQWCLKNGVSLIPPKGYSGQDFDWADYHKQHGAQEAPPFCFRNTSFSRGFTKNMKLE 415
                                                                                                                                                                                                                                                                                                                                                                         215 GGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHA 273
                                                                                                                                                                                                                                                                                                                                                          334 AVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQ-WVDCESPDIYPVGWCELTGYQLQ 392
62
                                                                                                                                                                           --MAHH--PIFRKIYCDAVPY----LFKKVRAVYTE
                                                                                                                                                                                                       246 CQE-----NKYRMDPPSEIYPLKMASEWKCTLEKSLIDAAKFPLPMEVFKDHADLRSH
                                                                                                                                                                                                                                                                                               IFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLE
                                                                                                                                  115 -QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLY---EDGDSDDDFWCHMMSPLIHPVGW
GMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGW
                                                        CAINSKILVPPRTIHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                  393 PPVAAEPATPLKAKEAT---KKKKKQFGKKRKIPPT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 44757; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #14389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG14398 standard; Protein; 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167
                                                                                                                                                                           171 SRRVGHGIKMSERRSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS78585.
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ABG14398
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          polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymurlectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating in equality of the polypeptide and polymucleotide sequences have applications in dispostics, forensics, gene mapping, identification of mutations in chaptoric for generation generated and produce other types of data and products dependent on DNA and amino acid sequences of the invention.

Oute: The sequence dispondences of the invention.

Oute: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                 IHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVIGGRIRLIYEDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPTFR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory; immunosuprressive; osteopathic; cytyseptuae; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; acancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; barcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia; psoriasis; hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                                                                                          14 PSRV----ALEQECGYNALLRYEGFENDSGLDFWCNICGSDIHPVGWCAASGKPLVPPRT
                                                                                                                                                                                                                                                                                                                                                                            PSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAINSKILVPPRT
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDDT; human; disease detection and treatment molecule polypeptide;
polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome
                                                                                                                                                                                                                                                                                                                                                47; Indels 12;
                                                                                                                                                                                                                                                                                                                       Length 205;
                                                                                                                                                                                                                                                                                                                   21.9%; Score 587; DB 22;
56.1%; Pred. No. 2.8e-52;
iive 28; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU11746 standard; Protein; 538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MDDT polypeptide SEQ ID 693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIYCDAVPYLFKKVRAVY 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001; 2001US-279619P.
29-MAR-2001; 2001US-280067P.
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                                                                                                                                                                                                                                                                                                                                   Local Similarity 56.1
nes 111, Conservative
                                                                                                                                                                                                                                                                                           205 AA;
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                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                       Query Match
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopothic, cytostatic, anti-HIV, haemostatic, nephrotropic, contemporatic, anti-HIV, haemostatic, nephrotropic, or continuation and heparcorropic activity. The polymucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are principlerative disorders (e.g. cancers including adenocarcinoma, proliferative disorders (e.g. cancers including adenocarcinoma, lumphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's syndromes, inflammathon, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABU11450-ABU11845 represent the MDDT polymucleotides encoded by ABU11450-ABU11845 represent the MDDT polymucleotides encoded by ABU11450-ABU11845 represent did not form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic form part of the printed to the vipo int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis
                                                                                                                                                                                                                                                                                                                            ran AB, Dahl CR, Gietzen D, Chinn J;
Yu JY, Tuason O, Yap PE, Amshey SR;
Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
Lewis SA, Chen AJ, Panzer SR, Harris B;
Lo A, Lan RY, Urashka ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 693; 339pp + Sequence Listing; English
16-MAY-2001; 2001US-291280P.
17-MAY-2001; 2001US-291829P.
17-MAY-2001; 2001US-291849P.
19-UUN-2001; 2001US-299428P.
20-UUN-2001; 2001US-299776P.
20-UUN-2001; 2001US-299776P.
                                                                                                                                                                                                                                                                                                                                        Tran AB,
                                                                                                                                                                                                                                                              (INCY-) INCYTE GENOMICS INC.
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Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                Daffo A, Jones AL, Trar Dufour GE, Hillman JL, Daugherty SC, Dam TC, Peralta CH, David MH, Flores V, Marwaha R, L
                                                                                                                                                                                                                                                                                                                                    Jones AL, Tra
Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-058431/05.
N-PSDB; ABX34736.
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447
   HFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA-AEPAT-----PLKAKEATK 410
                                                                                                                                                                328 TRISKYSFHHRKCPTPGCDGSGHVTGKFTAHHCLSGCPLAER--NOSRLKAELSDSEASA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antiamemic; antiporaticic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Cxchn; a disease; acquired immunodeficiency syndrome; AIDS; goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified disease detection and treatment molecule proteins and polynuclectides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis
                              -----PTKTRPLRQGSKKPLLEDDPQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뗦
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GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
YEY SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin F
A CH, David MH, Lewis SA, Chen AJ, Penzer SR, Harris B;
V, Marwaha R, Lo A, Lan RY, Urashka ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                             ABU11833 standard; Protein; 538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MDDT polypeptide SEQ ID 780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2001US-279619P.
; 2001US-280067P.
; 2001US-280068P.
; 2001US-29180P.
; 2001US-291849P.
; 2001US-299428P.
; 2001US-299428P.
; 2001US-299428P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                               KKKKQFGKKRKRIP-
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N-PSDB; ABX34823.
                                                                                                                                                                                                                            RK 449
                                                                                                                                                                                                                                                                               kk 387
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29-MAR-2001;
29-MAR-2001;
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Peralta CH,
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This invention describes a novel disease detection and treatment molecule bylypetide (MDIT) which has anti-inflammatory, immunosupressive, osteopathic, cytostatic, anti-inflammatory, nephrotropic, antipaoriatic and hepatotropic activity. The polynucleotides

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 HFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA-AEPAT-----PLKAKEATK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for disgnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's sisaese, acquired immunodeficiency syndrome (AIDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABU11450-ABU11845 represent the MDDI polynucleotides encoded by ABU11450-ABU11845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed especification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 TRTSKYSFHHRKCPTPGCDGSGHVTGKFTAHHCLSGCPLAER--NQSRLKAELSDSEASA 385
                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GMKLEGI--DPQHPS-MYFILIVAEVCGYRLRIHFDGYSE--CHDFWVNANSPDIHPDAGW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 CAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYP---FRQGMRL
                                                                                                                                                                                                                                                                                                                                                                                                                      3 GMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 FEKTGHKLOPPKGYKBEEFSWSOYLR----STRAQAAPKHLFVSOSHSPPPLGFQVGMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 MSERRSDWAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 NWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 KKKKQPGKKRKRIP----------PTKTRPLRQGSKKPLLEDDPQGA
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                                                                                                                                                                                                                                                                                                                                                                           Indels 156;
                                                                                                                                                                                                                                                                                                                                 19.0%; Score 510; DB 24; Length 538; 27.4%; Pred. No. 1.3e-43; vative 50; Mismatches 144; Indels 156
polypeptides of the invention can be used for
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Matches 132; Conservative
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Job time : 49 secs
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/cgm2_6/ptodara1/jaa/6A_COMB.pep:*
/cgm2_6/ptodara1/jaa/6B_COMB.pep:*
/cgm2_6/ptodara1/jaa/eTruS_COMB.pep:*
/cgm2_6/ptodara1/jaa/PcTruS_COMB.pep:*
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1-08-936-135-8
1-08-936-135-10
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 4, Application US/08852153
Sequence 4, Application US/08852153
Sequence 4, Application US/08852153
Sequence 4, Application US/08852153
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chirch Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 KVVIPKNPYPASDVNTEKPSIHSSTKTVLEHOPGQRGRKPGKRGKTPKTLISHPISAPS 236
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216 PPGTKVVIPKNPYPASDVNTEKPSIHSSTKTVLEHQPGQRGRKFGKKRGRTPKTLISHPI 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 KNDIELTPPKGYEAQTFNWENYLEKTKSKA - - APSRLFNWD - - CPNHG - FKVGMKLEAVD
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                                           425 --PTKT-RPL-----RQGSK-KPLLEDDPQGARKISSEPVP 456
                                                                                  276 SAPSKTAEPLKFPKKRGPKPGSKRKPRTLLNPPPASPTTSTPEP 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 353.5; DB 2; 36.1%; Pred. No. 1.1e-30; tive 30; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY.
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: PLOPS/MS-F
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GULh, JOSEPH H.
REGISTRATION NUMBER: 31,261
REPERENCE/DOCKET NUMBER: 122.
TELEPHONE: (510) 923-3888:
TELEPAK: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Matches 101; Conservative
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STATE: Californi
COUNTRY: U.S.A.
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APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                      187 PPGTKVVIPKNPYPASDVNTEKPSIHSSTKTVLEHQPGQRGRKPGKKGRTPKTLISHPI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 FEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 TFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKA--APSRLFNMD--CPNHG-FKVGMKL 332
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    67 GNCEKNGGMLQPPLGFRLNASSWPMFLLKTLNGAEMAPIRIFHKEPPSPSHNFFKMGMKL 126
                                                                                                                                  ------KOFGKKRKRIP----- 424
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                                             BAVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQ
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                                                                                                                                                                                                                                                              247 SAPSKTAEPLKFPKKRGPKPGSKRKPRTLLNPPPASPTTSTPEP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
CMDFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/852,153
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13.3%; Score 357.5; DB 2;
Best Local Similarity 35.9%; Pred. No. 4.5e-31;
Matches 102; Conservative 31; Mismatches 102;
                                                                                                                                  PP--VAAEPATPLKAKEATKKKK-----
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                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08852153
Patent No. 5914266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guth, Joseph H.
REGISTRATION NUMBER: 31,261
REFERENCE/DOCKET NUMBER: 122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 4, 2004, 09:08:22; Search time 39 Seconds (without alignments) 2657.544 Million cell updates/sec

Title: Perfect score:

US-10-031-915-36 2683 1 MKGMKVEVLNSDAVLPSRVY.......KASSPELFVSVENIKQETDD 495 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

801455 seqs, 209382283 residues

Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

todata/1/pubpaa/USO9E_TOGOTE_PD: todata/1/pubpaa/USO9C_FUBCOMB.pep: todata/1/pubpaa/USO9C_FUBCOMB.pep: todata/1/pubpaa/USO0AE_PUBCOMB.pep: todata/1/pubpaa/US10A_FUBCOMB.pep: todata/1/pubpaa/US10C_FUBCOMB.pep: todata/1/pubpaa/US10C_FUBCOMB.pep: 6/ptodata/1/pubpaa/U310C_PUBCOMB.pep. 6/ptodata/1/pubpaa/U310 NEW PUB.pep.* 6/ptodata/1/pubpaa/U360 NEW PUB.pep.* 6/ptodata/1/pubpaa/U360_PUBCOMB.pep.* ptodata/1/pubpaa/USO7_NEW_PUB.pep:"
ycodata/1/pubpaa/PCTUS_PUBCOMB.pep
ptodata/1/pubpaa/USO8_NEW_PUB.pep:"
ptodata/1/pubpaa/USO8_PUBCOMB.pep:" PUBCOMB. pep Published Applications Ab: * /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: pubpaa/US09A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2556, Ap	Sequence 4101, Ap	Sequence 1824, Ap	Sequence 56, Appl	Sequence 68, Appl	Sequence 3512, Ap	Sequence 5, Appli	Sequence 71, Appl	Sequence 72, Appl	Sequence 27484, A	Sequence 38826, A	Sequence 30438, A	Sequence 2262, Ap	Sequence 3204, Ap	Sequence 2539, Ap
	ΠD	US-10-094-749-2556	US-10-108-260A-4101	US-10-264-237-1824	US-09-789-919-56	US-09-872-523-68	US-10-104-047-3512	US-09-872-523-5	US-09-872-523-71	US-09-872-523-72	US-10-029-386-27484	US-09-864-761-38826	US-10-029-386-30438	US-10-104-047-2262	US-10-104-047-3204	US-10-264-049-2539
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	Query Match Length DB	705	526	329	631	410	623	498	498	498	78	77	77	427	406	217
æ	Query Match	99.9	81.4	62.9	52.6	51.7	18.5	18.4	18.4	18.1	16.4	15.5	15.5	14.8	14.5	13.9
	Score	2679	2185	1688	1410	1387	495.5	494.5	493.5	486.5	440	417	417	398	389.5	373.5
	Result No.		7	m	4	ω	9	7	00	ወ	10	11	12	13	14	15

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US-09-801-574-12 US-09-872-523-7 US-10-8872-523-70 US-10-204-887-93 US-09-872-523-69 US-09-872-523-10 US-09-872-523-10 US-10-104-047-2159 US-09-764-868-1009 US-09-872-523-12 US-09-872-523-12 US-09-872-523-12	US-09-872-523-115 US-09-864-761-38862 US-09-872-523-113. US-09-872-523-113. US-09-864-761-36870 US-09-864-761-36870 US-09-864-761-36870 US-09-864-761-42641 US-10-03-8864-761-42641 US-09-864-761-42641 US-09-864-761-38882 US-10-369-493-3803 US-10-369-493-3803 US-10-369-493-3803 US-09-895-943-13304 US-09-895-943-13304 US-09-895-943-13304 US-09-895-943-13304 US-09-895-943-13304 US-09-895-943-13304 US-09-895-943-13304 US-10-008-566-4	
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AL I GNMENTS

APPLICANT: TAMECHIKA, ICCHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SCHIKAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749 2001-328381 Sequence 2556, Application US/10094749 Publication No. US20030219741A1 GENERAL INFORMATION: ISOGAL, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI OTSUKA, KAORU NAGAI, KEIICHI NAGAI, KEIICHI IRIE, RYOTARO

PRIOR APPLICATION NUMBER: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2556
TANDER: 705

TYPE: PRT
CORGANISM: Homo sapiens
US-10-094-749-2556

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LOCATION: (185)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRATURE:
NAMB/KEY: MISC FEATURE
LOCATION: (223)
CTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1824
                                                                                                                                                               360 CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIBLTPPKGYBAQTFNW 419
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240 VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIRM
                                                                                          300 SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
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                                                          SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PAL31P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PATENTION NUMBER: US 60/205,515
FRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PATENTIN Ver. 3.1
SEQ ID NO 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.9%; Score 1688; DB 12; Length 329;
99.0%; Pred. No. 2.8e-160;
iive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                361 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAA 397
                                                                                                                                                                                                                                                                                                                          ; Sequence 1824, Application US/10264237; Publication No. US20040009491A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE LOCATION: (185)
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US-10-264-237-1824
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                       Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4101, Application US/10108260A; Publication No. US20040005560A1; Publication No. US20040005560A1; Publication No. US20040005560A1; APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFERENCE: H1-A0106; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 4101
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATPL
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                                                              ;
                    Score 2679; DB 12;
Pred. No. 4.5e-259;
0; Mismatches 1;
                  99.9%;
Similarity 99.8%;
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Matches 397; Conservative
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ORGANISM: Homo sapiens
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US-10-108-260A-4101
                                                          494;
                    Query Match
Best Local S:
Matches 494
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CURRENT APPLICATION NUMBER: US/09/872,523
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                                                                                                           LENGTH: 410
                                                                                          SEQ ID NO 68
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                                                                                                                   Sequence 56, Application US/09789919
Sequence 56, Application US/09789919
GENERAL INFORMATION
APPLICANT: Lemischka, Ihor
APPLICANT: Moore, Kateri
TITLE OF INVENTION: GENES THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: CELLS AND USES THEREOF
TITLE OF INVENTION: 2275-1-005
CURRENT APPLICATION NUMBER: US/09/789,919
CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
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APPLICANT: Davison, Ewa M.
APPLICANT: Davison, Ewa M.
APPLICANT: Lu, Xiaowei
TITLE OF INVENTIOR: A Tumor Suppressor Pathway in C. Elegans
FILE REFERENCE: 01997/536002
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                            52.6%; Score 1410; DB 9; 56.2%; Pred. No. 5.1e-132; tive 67; Mismatches 122;
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Patent No. US20020137906A1
GENERAL INFORMATION:
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Best Local Similarity 56.2<sup>3</sup>
Matches 263, Conservative
           ENYLEKTKSKA 311
                                        301 ENYLEKTKSKA 311
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TILLE OF INVENTION: No. US20030236392Ale1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR PILING DATE: 2002-03-25
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3512
LENGTH: 623
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                                                                                                                                                                                                                                                                                                      51.7%; Score 1387; DB 10;
62.6%; Pred. No. 5.4e-130;
cive 56; Mismatches 84;
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36.6%; Pred. No. 2.1e-40;
tive 53; Mismatches 118
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,802
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030236392A1
GENERAL INFORMATION:
                                                                                                                                                                                               7 TYPE: PRT
7 ORGANISM: Caenorhabditis elegans
US-09-872-523-68
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 62.69
Matches 248; Conservative
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; ORGANISM: Homo sapiens
US-10-104-047-3512
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Best Local Similarity
Matches 121; Conserv
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109 MPSQERLDKFKVILISKRVGLRLEAADMCENQFICPATVKSVHGRLINVNFDGWDEEFDE 468
                               370 WVDCESPDIYPVGWCELTGYQLQPP 394
                                                                469 LYDVDSHDÍLPIGWCEAHSÝVLÓPP 493
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                                                                                                                                               Sequence 71, Application US/09872523
Patent No. US20020137906A1
GENERAL INFORMATION:
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Patent No. US20020137906A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-872-523-71
                                                                                                                                                                                                APPLICANT: Horvitz, H. Robert
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Best Local Similarity 29.7%
Matches 132; Conservative
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VIGGRIRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPT-FRK- 195
                                                              ----AVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 FIFPVGFAAVNGYQLNAKKEYIEHTNKIAQAIKNGENPRYDSDDVTFDQLAKDFIDPMIW 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 KKVRAVYTEGGWFEEGMKLEAIDPL--NLGNICVATV---CKVLLDGYLMICVDGGPSTD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 GLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 --DSFPIHINNTFMFPVGYAEKYNLELVPPDEFKG-TFRWDEYLEKESAETLPLDLFK-P 408
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                                  ---HIPKGYRKD
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                                                                                                                                                              219 ED-RILVHFDNW--DDSYDYWC-DVNSPYVQPVGWCQENGRTLIAPQGYPNPENFSWTEY
                                                                                                                                                                                              LEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHFDGW
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APPLICANT: Lu, Xiaowei
TITLE OF INVENTION: A Tumor Suppressor Pathway in C. Elegans
FILE REFERENCE: 01997/536002
CURRENT APPLICATION NUMBER: US/09/872,523
CURRENT FILING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 29.7%; Pred. No. 1.9e-40;
Matches 132; Conservative 81; Mismatches 149; Indels
                               VCGYRLRLHFDGYLSCYDFWTNAGSPDIHPVGWCEKTKHEL-
                                                                                                                                                                                                                                                                                364 DSEYDOWVDCESPDIYPVGWCELTGYOLOPP 394
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
IENGTH: 498
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PRIOR FILING DATE: 2000-06-02
                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09872523
Patent No. US20020137906A1
GENERAL INFORMATION:
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ORGANISM: Caenorhabditis elegans
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                                                                --IYCD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 KKVRAVYTEGGWFEEGMKLEAIDPL--NLGNICVATV---CKVLLDGYLMICVDGGPSTD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 RKVKV------GQKFELIDPLAQQFNNLHVASILKFCKT--EGYLIVGMDGPDALE 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ILVPPRTIHAKF-TDWKGYLMK----RLVGSRTLPVDFHIKMVESMKYPFRQGMRL
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APPLICANT: Davison, Eva M. Applicant: Davison, Eva M. APPLICANT: Davison, Eva M. APPLICANT: Davison, Eva M. Tumor Suppressor Pathway in C. Elegans PILE REFERENCE: 01997/536002 (URRENT APPLICATION NUMBER: US/09/872,523 (URRENT FILING DATE: 2001-06-01 PRIOR APPLICATION NUMBER: US 60/208,802 PRIOR FILING DATE: 2000-06-02 RIOR FILING DATE: 2000-06-02 SPIGOR FILING DATE: 78 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.4%; Score 493.5; DB 10; Length 29.7%; Pred. No. 2.4e-40; ive 81; Mismatches 149; Indels
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1487, App 1855, App 1856, App 1868, Ap 1888, Ap

Sequence Seq

36, Appl 2539, Ap

Sequence Sequence Sequence Sequence Sequence Sequence

Feb

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GENERAL INVENTION:

APPLICANT: Venter: J. Craig

APPLICANT: Venter: J. Craig

APPLICANT: Venter: J. Craig

APPLICANT: Venter: J. Craig

TITLE OF INVENTION: DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOD728

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT PILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/160,332

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 4300-03

SOFTWARE: PRESEED FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 GMKVEVENTDCDSIEVIQPGQTPTSFWVATILEIKGYKALMSYEGFDTD-SHDFWVNLCN
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US-10 648-512-22

US-10-648-512-32

US-10-648-512-32

US-10-679-063-17795

US-10-679-063-17795

US-10-679-063-17795

US-60-495-114-148

US-60-495-114-148

US-60-495-114-148

US-60-495-114-148

US-60-495-114-148

US-60-495-114-148

US-60-500-337-2394

US-60-500-337-2396

US-60-500-337-2396

US-60-500-337-2396

US-60-500-337-2396

US-60-500-337-2396

US-60-500-337-2396

US-614-1504-39579
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US-09-614-150A-38841
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LENGTH: 891
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693, App
780, App
12672, Ap
724, App
20184, Ap
800, App
1851, Ap
800, App
25, Appl
25, Appl
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25, Appl
26, Appl
26, Appl
27, Appl
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2525, Ap
42, Appl
6006, Ap
49488, A
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1675.070 Million cell updates/sec
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2683
1 MKGMKVEVLNSDAVLPSRVY.......KASSPELPVSVENIKQETDD 495
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US00_NEW_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-473-040-693
US-10-473-040-693
US-10-473-040-724
US-10-473-040-724
US-10-473-040-550
US-09-614-150A-20184
US-60-1851
PCT-US03-21379-80
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US-09-614-150A-31704
US-10-425-114A-67814
US-10-425-114A-65213
US-10-739-930-7654
US-60-490-890-2525
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US-09-614-150A-6006
US-10-425-114A-49488
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                                                                                                                                                                                                                                                                                                                                                                 376054 seqs, 77831530 residues
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                                                                                               - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 200000000
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Match Length
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No.
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14;

68; Gaps

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Sequence 647, Application US/10719993
GENERAL INFORMATION:
GENERAL INFORMATION:
THE CF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FIFTH REPREBENCE: LO1001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 647
LENGTH: 894
921 PRLYCVATVARVVGRLLKVHFDGWTDEYDQWLDCESADIYPVGWCVLVNHKLEGPPRVAH 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 -QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLY---EDGDSDDDFWCHMMSPLIHPVGW 170
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                                                                                                                                                                                                     PRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               981 QQAPKPAPKPKIQRKRKPKKGAAGGK----TPTDNNTQSVKSRTIALKTTPH-----
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                                                                                                  GHGI-----KWSERRSDMAHHPTFRKIYCDAVPYLFK---KVRAVYTEG--GWFEE
                                                                                                                                                                                                                                                                                                                                                             COKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLME
                                                                                                                                                                                                                                                                  GMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-719-993-647
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US-10-719-993-647
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT PILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-13

PRIOR PILING DATE: 2090-0-1-12

PRIOR PILING DATE: 2000-0-1-2

PRIOR PILING DATE: 2000-0-1-3

PRIOR PILING DATE: 2000-0-3

PRIOR PILING DA
  220
                                                                                                            GHNLAAPQDYLBRMLAGREAMIEVHED-----DATIELFKMNFTFDEYYSDGKTNSFVE 448
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                                                                                                                                                                                                                                                                  COKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLME 339
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                                                                            GHGI-----KVRAVYTEG--GWFEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-614-150A-27069
; Sequence 27069, Application US/09614150A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Venter, J. Craig APPLICANT: et al.
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US-09-614-150A-27069
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 4, 2004, 09:05:51; Search time 20 Seconds (without alignments) 2380.175 Million cell updates/sec

US-10-031-915-36 2683 1 MKGMKVEVLNSDAVLPSRVY......KASSPELPVSVENIKQETDD 495 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		_	Sor		٦	nebulin, skeletal	mating type silenc	DNA topoisomerase	DNA topoisomerase		FIM protein [impor	polynucleotide ade	polynucleotide ade	microtubule-associ	neurofilament prot	×	Ω.	hypothetical prote	hypothetical prote	hypothetical prote	probable histone a	phosphoprotein pho	Cys-rich protein R	myosin-light-chain	a١	histone H1 - maize	hypothetical prote	፟	hypothetical prote
SUMMARIES	ΙD	T23964	T12525	T13797	T14794	F6421.7	S55024	T09481	G86586	D72038	S18642	T45119	S17875	S17925	A33319	B43427	T49475	F91286	B86128	F84912	T47381	T39004	T45058	T09483	JG0197	H86440	S26826	850	F70435	4
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hematopoietic line	hypothetical prote	nypothetical prote	protein F18014.25	related to gastric	zinc finger protei	hypothetical prote	histone H1, stress	neurofilament trip	cytochrome P450 AL	probable Na+/H+ an	neurofilament trip	membrane klotho pr	ankyrin 2, neurona	ftsK homolog - Str	histone H1, drough
807633	T27100	T18738	H86327	T49813	S27802	T19450	T07035	QFHUH	JS0724	E84431	A43427	JC5925	S37431	T35683	865059
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30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

					18	89	245	119	305	163	365	205	425	260	473	320	529
	al protein R06C7.7 - Caenorhabditis Caenorhabditis elegans -OCE-1999 #sequence_revision 15-Oct n: T23964	the F number T2396 Telimir	A;Residues: 1-619 <wil> A;COSS-references: EMBL:Z71266; PIDN:CAA95838.1; GSPDB:GN00019; CESP:R06C7.7 A;Experimental source: clone R06C7 C;Genetics:</wil>	. A;Gene: CESP:R06C7.7 A;Map position: 1 A;Introns: 121/3; 182/3; 238/2; 270/3; 547/3; 594/2	Query Match 18.4%; Score 494.5; DB 2; Length 619; Best Local Similarity 29.7%; Pred. No. 2.1e-33; Matches 132; Conservative 81; Mismatches 149; Indels 83; Gaps		Db 193 NCDSIQVRWFARIEKVCGYRVLAQFIGADTKFWLNILSDDMFGLANAAMSDPN ;		Db 246 MDKIVYAPPLAINBEYQNDMVNYVNNCIDGEIVGQTSLSPKFDEGKALLSKHRFKVGQRL	Cy 120 EVVDKSQVSRTRMAVVDTVIGGRIRLLXEDGDSDDDFWCHMWSP	Db 306 ELLINYSINSTEIRVARIQEICGRRMIVSITKKDFPESLPDADDDRQVFSSGSQYMIDEGSF 3	CY 164 LIHPVGWSRRVGHGIKWSERRSDMAHHPTFKKIYCDAV-PYLF :	Db 366 FIFPVGFAAVNGYQLNAKKEYIEHTNKIAQAİKNGENPRYDSDDVTFDQLAKDPIDPMIW	QY 206 KKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTD 3	Db 426 RKVKVGQKFELIDPLAQQFNNLHVASILKFCKTEGYLIVGMDGPDALE	Qy 261 GLDWFCYHASSHAIFPAIFCQKNDIBLIPPKGYBAQIFNWBNYLBKTKSKAAAPSRLFNMD 3	Db 474 DSPPIHINNTFMPPVGYAEKYNLELVPPDEFKG-TFRWDEYLEKESAETLPLDLFK-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAINSKILVPPRTIHAKFIDWKGYLMKRLVGSRTLP--VDFHIKMVESM--KYPFRQGMR 118
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C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                           A,Cross-references: EMBL:X80839; NID:g530289; PIDN:CAA56811.1; PID:g3421009
C,Genetics:
A,Cross-references: FlyBase:FBgn0002441
A,Introns: 210/3; 746/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908 CDETARVLQAPKDYNSERFSWSRYLVK--TGGKAAPRALFGHLNMOOOMDVRNGFAVGMH
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                                                                                                                                                                                                                                                                                                                                                                                                             222 MKLEAIDPINLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQ
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                                                                                                                                                                                                              Query Match
15.0%; Score 402; DB 2; Length 1477;
Best Local Similarity 21.9%; Pred. No. 4e-25;
Matches 117; Conservative 83; Mismatches 159; Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39
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R;Kochrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, August 1999

A;Reference number: Z18180

A;Accession: T14794

A;Acce
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C;Species: Drosophila melanogaster
C;Date: 13-Mug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13797
R;Wismar, J.; Loeffler, T.; Habtemichael, N.; Vef, O.; Geissen, M.; Zirwes, R.; Altmeyer
R;Wismar, J.; Loeffler, T.; Habtemichael, N.; Vef, O.; Geissen, M.; Zirwes, R.; Altmeyer
A;Title: The Drosophia melanogaster tumor suppressor gene lethal(3)malignant brain tumor
A;Reference number: Z17760; MUD: 96100389; PMID: 8555106
A;Accession: T1397
A;Accession: T1397
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 AVRGSYLWIQLEGSKKPIPECIVSVESMDIFFLGWCETNGHPL-----STPRRAR-V 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 AFQDSLSTWIVTVVVENIGGRIKCHYYEGESSDNYEHWLYYLDPFLHHVGWAAQQGYELQP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 PPGYPSQDFDWADYLKQCGABAAPQRCFPPLISEHEFKENWKLEAVNPILPEBVCVATIT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 NSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYP---FRQGMRLEVV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SERRSDMAHHPTFRKIYC-----DAVP-YLF--KKVRAVYTEGGWFEEGMKLEAIDPL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 NLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATFCQKNDIELTP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVVHRLLSIHFDGWDSEYDQW-VDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 TKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEH 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 YKORKIAVVOPEKOVPSSRT--VHEGLRN------ÖELNSTESVMINGKYCCPKIYFNH 397
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                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 PSAIRHLKNEAEWQEILAKVKEEEEEPLPSYLFKDKQVIGIHT-+--FSVNMKLEAVDPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NKYLEAPEGIRDKVSDWDEFLRQTLIGACSPPVPL-LEGLRNGRNPLDLIAPGSRLECQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                   RESULT 2
T12525
hypothetical protein DKFZp434L243.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Dete: 23-Jul.1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul.
C;Accession: T12525
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, June 1999
A;Reference number: 217524
A;Accession: T12525
A;Sterus: preliminary
A;Molecule type: mRNA
A;Residues: 1-711 < **MAN
A;Cross-references: EMBL:ALO80140
A;Experimental source: adult testis; clone DKFZp434L243
C;Genetics:
A;Note: DKFZp434L243.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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                                      590 LYDVDSHDILPIGWCEAHSYVLQPP 614
394
370 WVDCESPDIYPVGWCELTGYQLQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 LDVASP--DKASSPELPVSV 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 30.29
Matches 133, Conservative
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February 4, 2004, 09:05:51; Search time 39 Seconds (without alignments) 3275.283 Million cell updates/sec
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                                                                                                                                                                                             US-10-031-915-36
2683
1 MKGMKVEVLNSDAVLPSRVY......KASSPELPVSVENIKQETDD 495
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                         OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
6: sp_invertebrate:*
6: sp_mammal:*
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Maximum DB seq length: 2000000000
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Sp_rodent:*
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Perfect score:
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	Description	Osphds musculu	O8vel2 mus musculu	_	Ognaul homo sapien	O9vk33 drosophila	Oscib4 mus musculu	Q96c73 homo sapien	Oguhi3 homo sapien	Oghcf5 homo sapien	O9jmd1 mus musculu	Q9jmd2 rattus norv	Oscfs1 mus musculu	O961m7 homo sapien	OSPID7 mus musculu	Osiuv7 homo sapien	Q21769 caenorhabdi
SUMMARIES	. ОІ	QBBHD5	Q8VE12	QBBZY2	TOXN60	_		_	_	Q9HCF5	Q9JMD1	Q9JMD2	QBCFS1	Q96JM7	Q8BLB7	QBIUV7	Q21769
	DB	1	11	11	4			4			11						Ŋ
	* Query Match Length DB	703	464	411	410	1243	359	998	866	904	863	863	591	781	883	772	612
•	% Query Match	90.4	52.9	52.1	52.0	41.4	40.2	23.1	23.1	22.8	22.5	22.3	22.3				
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המעים שהעיבת פורתפה	homo sapie	homo	homod		drose	Q9ukm6 homo sapien	home	Q9ukm5 homo sapien	OHO	Q9ugr0 homo sapien	mus	muse m	Osbycs musculu	Q9n3q7 caenorhabdi	Q99mw4 mus musculu	Q9vha0 drosophila	Q9w6r7 fugu rubrip	Q9ntw3 homo sapien	mus	OBbhz8 musculu		Q8iwd0 homo sapien	Q8bmn8 musculu	ошос	рошо	ошог	Q8c0g4 mus musculu	Q8spm4 bos taurus
Q.T.T.20	OBIXS3	08NA19	Q9Y4Q9	09VB52	076931	Q9UKM6	Q96GD3	Q9UKM5	Q8WU48	Q9UQR0	1 Q9JME0	Q8K214	BDAC8	Q9N3Q7	_ Q99MW4	Q9VHA0	3 Q9W6R7	Q9NTW3	Q8BKW1	OBBHZ8	. Q8BG70	QBIWDO	CBBMIN8	075996	096LH0	Q8WX46	Q8C0G4	Q8SPM4
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α.	18.5	18.5	17.6	15.0	15.0	13.3	13.3	13.2	13.2	13.1	13.0	13.0	12.7	12.4	12.3	12.2	12.2	12.1	10.0	ω ω	o 4.	9.4	8.2	7.7	7.3	5.9	4.8	4.5
499	'n	ദ	471	402	402	357.5	357.5	353.5	353.5	351	349	349	340	332	330	327	326.5	323.5	269	255.5	252.5	226.5	221	206	197	158	130	121
17	18	19	50	21	22	23	24	52	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

OSEHUS.	QBBHDS PRELIMINARY; PRI; 703 AA.:	Q8BHD5; 01-MAR-2003 (TrEMBLrel. 23, Created)	(TrEMBLrel. 23,	AR-2003. (TrEMBLrel. 23, Last	H-L.	$\overline{}$	Metazoa; Chordata;	ilia; Eutheria; Rodentia;	100001=	יין וויוויייייייייייייייייייייייייייייי		STANTINGO DO STINONE BOILD SKIII)	MEDIANDE ZASSAGRAZIA FUDMEQ=1Z466851; The Daymon Commentation	THE PARIOR CONSOLLING. PRESENCY CARNIN DRESS I G. II DEST.	initial contains aspitation research stody finase i a ii	of the mouse transcriptome pased on functional annotation		K029115;	036510; BAC29456.1;	SEQUENCE 703 AA; 78970 MW; 2E9B5DF5BFCEAFF9 CRC64;	Query Match 90.4%; Score 2426; DB 11; Length 703;	Stuniarity 67:3%; 3; Conservative 23	1 MKGMKVEVINSDAVLPSRVYWIASVIQTAGYRVLLRYBGFENDASHDFWCNLGTVDVHPI	211 MKGMKVEVLNSDAVLPSRVYWIATVIQAAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI	61 GWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE		271 GWCAINSKILVPPRTIHAKFTDWKSYLMKRLVGSRTLPADFHIKMVESMKYPFRQGMRLE	121 VVDKSQVSRTRNAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIRM	
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243 RKVLADGFLMIGIDGSBAADGSDWFCYHATSPSIFPVGFCEINMIELTPPRGYTKLPFKW 302
                                                                                             DGWDSBYDQWVDCESPDIYPVGWCELIGYQLQPPVAAEPATPLKAKEATKKK-KKQFGKK 419
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MEDIJNE=22354683; PubMed=12466851;
The FANTOM CONSortium,
The RANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of the Marty Consortium,"
Nature 420:663-673 (2002)
EMBL; AK033238; BAC28206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÷.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Last Weakly similar to H-L (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                 Coll. MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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VVDKTQVSRTRMAVVDTVIGGRLRLLYEDGDSDDFWCHMWSPLIHPVGWSRRVGHGIKM 390
                                                                  CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
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                                                                                                                                                                                                                                                                                                                KRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSP 480
                                                                                                                                                                                                                                                                                                                                                                                                      70 WCAASGKPLVPPRTVQHKYTNWKAFLVKRLTGAKTLPPDFSQKVSESMQYPFKPCMRVEV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 VDKSQVSRTRMAVVDTVIGGRLRLLYEDG-DSDDDFWCHWWSPLIHPVGWSRRVGHGIKM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WCAINSKILVPPRIIHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLEV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                451 CKVLLDGYLMICVDGGPSTDGSDWFCYHASSHAIFPATFCQKNDIELTPPKGYETQPPAW
                                                                                                                                                                                                                                  SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGWKLEAIDPLNLGNICVATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
                                                                                                                                                                                                                                                                                            DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEATKKKKKQFGKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020018; AAH20018.1; -.
MGD; MGI:2143377; AA408199.
InterPro; IPR004092; Mbt.
Pfam; PP02820; mbt; 4.
SMART; SM00561; MBT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 464 AA; 52721 MW; 31E5C041592BE874 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Similar to hypothetical protein FLJ20055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.9%; Score 1418; DB 11;
56.4%; Pred. No. 1.1e-126;
iive 67; Mismatches 121;
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689 QLPLPIESIKQERNN 703
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Ephydroidea; Drosophilidae; Drosophila
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                              NCBI_TaxID=7227;
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"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00062; BAA90919.1;
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.0%; Score 1395; DB 4; Length 410; Best Local Similarity 62.9%; Pred. No. 1.4e-124; Matches 249; Conservative 55; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 410 AA; 46717 MW; 6E9C09639AC02CF3 CRC64;
                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OMP-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ20055.
Homo sapiens (Human).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004092; Mbt. Pfam; PF02820; mbt; 4. SMART; SMON561; MBT; 4.
                                                                                 PRELIMINARY;
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                                               TUXN60
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RCANINGERRELEN, No. (LOWIG AND SHOKT ISOFCKNES).

RATAINGERRELEN, No. (LOWIG AND SHOKT ISOFCKNES).

RAMEDINGEZOURGO(G) FURNHEDEL TOTAINGER.

RAMEDINGEZOURGO(G) FURNHEDEL TOTAINGER.

RAMEDINGEZOURGO(G) FURNHEDEL TOTAINGER.

RAMEDINGEZOURGO(G) FURNHEDEL TOTAINGER.

RAMEDINGER P.G., ROGHER S.E., Richards R.A., Galle R.F.,

RAMEDINGER R.A., Lewis S.E., Richards B.R., Tahange N., Chan L.X.,

RAMEDING R.C., Rogers Y.-H.C., Blacap R.G., Chan L.X.,

RAMEDING R.C., Rogers Y.-H.C., Blacap R.G., Chan L.X.,

RAMEDING R.C., Rogers Y.-H.C., Blacap R.G., Change M., Pfeitfer B.D.,

RADIS R.M., Barus A., Berman B.P., Bhandari D., Borsley E.M.,

RAMEDIS R.M., Barus P.V., Berman B.P., Bhandari D., Borsley E.M.,

RADIS R.M., Barus P.V., Berman B.P., Bhandari D., Bolshakov S.,

RAMEDIS R.M., Bolcher A., Deng Z., Manys A.D., Dew I., Dietz S.M.,

ROGHON K., Doug L.E., Downes M., Dugarn Rocha S., Dunkov B.C.,

RAMEDIS R.M., Brungelian R.C., Ferraz C., Perriera S., Pleichann W.,

RAMEDIN R.J., Brungelian R.E., Garg N.S., Gelbart W.M., Classer K.,

RAMEDIN L., Harvey D., Helman T.J., Herrandez J.R., Houck J.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,

RAMEDIN L., Mattei B., McIntosh T.C., McLeod M.P., McIrng W., Lin X.,

RAMEDIS R.M., Poly M., Murphy B., Murphy L., Muzhy D., Lin Z., Liang Y., Lin X.,

RAMEDIS R.M., Pittenn G.S., Pan S., Pollard J., Palazzolo W., Pittenn G.S., Pan S., Pollard J., Palazzolo W., Sitten G.S., Van D. K., Nessen D.E.,

RAMEDIS R.M., Pittenn G.S., Pan S., Pollard J., Palazzolo W., Siden T.Y.,

RAMEDIS R.M., Podage T., Wolster R.N., Wanskern D.R., Wanskern D.R., Wanskern D.R., Wanskern D.R., Wanskern D.R., Wanskern S., Wang X.,

RAMEDIS R.M., Woodage T., Wolley K.C., Wu D.Y., Sun B.C., Siden-Kindon G.S., Pan S., Chopelor F., Wang X.,

RAMEDIS R.M., Woodage T., Wolley K., Weitseenbach J.,

RADIS R.M., Woodage T., Wolley K., Walskern B.C., Scheler F., Sahn H.,

REBEN R.M., REPRODUCES 2 ISOPRAS, A LONG FORM (SHOWN HERE) AND A

SHERL, Addis R.M., Woodage T., Wang W., Wang S., Wang S., Wang S., Wang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 VDVHPIGWCAINSKILVPPRTIHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           570 GMKVEVENTDCDSIEVIQPGQIPTSFWVATILEIKGYKALMSYEGFDTD-SHDFWVMLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GMKVEVLNSD-----AVLPSRV---YWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1243;
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43.4%; Pred. No. 9.7e-97;
tive 75; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50105; SAM_DOMAIN; 1.
Alternative splicing; Hypothetical protein.
VARSPLIC MISSING (IN SHORT ISOFORM).
SEQUENCE 1243 AA; 136036 MW; 35FC45F6298F5BAA CRC64;
                            (LONG AND SHORT ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0032475; CG16975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 234; Conservative
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InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02820; mbt; 4.
Pfam; PF00536; SAM; 1.
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SMART; SM00454; SAM; 1
[1]
SEQUENCE FROM N.A.
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62 WCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYP---FRQGMR 118
    337 LMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA 396
                                                                                          397 AEPATPLKAKEATKKK-KKQFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPV 455
                                                                                                                           294 QSSRBSQSASSKQKKKAKSQQYKGHKKMTTSQL-----KBELLDGEDYSFLHGASDQB 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDF--WCHMWSPLIHPVGWSRRVGH 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 LECQAPQDSLSTWIVTVVENIGGRLKLRYEGLESSDNYEHWLYYLDPFLHHVGWAAQQGY 227
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284 VDPWSPFGISPATVVKVPDEKYFLVEMDDLRPENHARRSFVCHADSPGIFPVQWSLKNGL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATVKRVVHRLLSIHFDGWDSEYDQW-VDCESPDIYPVGWCELTGYQLQPPVAAEPATPLK 404
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                              234 LMEPRLICVATVTRIHRLLRIHFDGWEESYDOWVDCBSPDLYPVGWCQLTGYQLQPPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GMKVEV-LNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 IDPLNLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATFCQKNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIKMSERRSDMAHHPTFRKIYC-----DAVP-YLF--KKVRAVYTEGGWFEEGMKLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 ELIPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Straubberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC014614; AAH14614.1; -.
InterPro; IPR004092; Mbt.
InterPro; IPR004092; Mbt.
Pfam; PF00280; mbt; 4.
Pfam; PF005816; SAM; 1.
SMART; SM00561; MBT; 4.
SWART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      866 AA; 98141 MW; DCE67BF35C413EB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.1%; Score 620.5; DB 4; larity 31.9%; Pred. No. 4.3e-50; Conservative 91; Mismatches 205;
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                             Q96C73;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                              | :|:|
347 SNGSATVYIKQE 358
                                                                                                                                                                                  PGEIIAVRVKEE 467
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similar to RU1.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 161; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Muscle;
                                                                                                                                                                                456
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279
                                                                                                                                                                                                       860
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                                                                                                                                                                                                                                                                                                                                                                                                                             395 -VAAEPATPLKAKEATKKKKKOFGKKRKRIPPTKTRPLROGSKKPLLEDDPQGARKISSE 453
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STRAIN=C57BL/6J; T1SSUE=Skin;
MFDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:533-573(2002).
EMBL; AK028503; BAC25982.1; -.
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		622,	622,	917,	419,	1658,	70682,	70683, A			293974	302414	293974	302414	22234	
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SUMMARIES	QΙ	US-10-117-722-622	US-10-037-270-622	US-10-094-749-917	US-10-264-237-419	US-10-108-260A-1658	US-10-027-632-70682	US-10-027-632-70683	US-10-027-632-70682	US-10-027-632-70683	US-10-027-632-293974	US-10-027-632-302414	US-10-027-632-293974	US-10-027-632-302414	US-09-918-995-22234	JS-09-789-919-55
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	% Query Match Length DB	2781	2781	3188	2663	2432	513	513	513	513	472	472	472	472	492	3590
	% Query Match	99.8	8.66	99.4	98.4	48.1	20.0	20.0	20.0	20.0	18.4	18.4	18.4	18.4	17.1	16.2
	Score	2550.8	2550.8	2538.8	2514.4	1227.8	512.2	512.2	512.2	512.2	471.2	471.2	471.2	471.2	438	413.8
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1 AGCACGTCCCACTCTATGACCAGTGGGAGGATGATGAAAGGGATGAAGGTGC 60

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4 WOOGOOOO HH HH H	RESULT 1 US-10-117-722-622 Sequence 622, Application US/1011722 SENERAL INFORMATION: APPLICANT: Liu, Chenghua APPLICANT: Asundi, Vinod APPLICANT: Asundi, Vinod APPLICANT: Dramand, Radoje T. TITLE OF INVENTION: No. US20030219744Alel TITLE OF INVENTION: No. US20030219744Alel TITLE OF INVENTION: No. US20030219744Alel TITLE OF INVENTION: No. US20030219744Alel TITLE OF INVENTION: No. US20030219744Alel FRICANT: APPLICATION NUMBER: US/10/117,722 CURRENT APPLICATION NUMBER: 09/620,312 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21 SOFTWARE: Dt FL_Genes Version 1.0 SEQ ID NO 622 LENGTH: 2781 TYPE: DNA ORGANISM: Homo sapiens FEATURE: TATES: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: CDS	Query Match Best Local S Matches 2552
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141 AGTGGGTGGACTGCGAGCACATCTACCCCGTCGGCTGAGCTCACCGGCT 1200	1501 TCAAGCAGAAACAGACGACTACTGCCTCCAGCCTCTGGCTTCTAGCTGGAAGCC 1501 TCAAGCAGGAAACAGACGACTGACTCCTGCCTCCAGCCTTCTAGCTGGAAGCC 1781 TCATGCAGGATTCTCTACCACCTCCTGCTCCAGCCTTCTAGCTTGAGACTGA 1620 TCATGCAGCTTTCTTCTACCACCACCACCACCACCACCACCACCACCA	1921 CCTGAACGAGTCATGTAAATTAAGTTCTAGAGCAGCTCTCTGAGCAGGATAAGGTCCCCT 1980

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Qy 2160 GCCTTGAGCTGCTTTGTGAGGACTGACTCCCATTTCCTAAAGGAAATGCCC 2219 Db 2231 GCCTTGAGCTGCTTTGTGAGGACTGACTCCCATTTCCTAAAGGAAATGCCC 2290 Qy 2220 CGGGGAGGAAATTGGAGAGAAGATGGCCTGAGTGCCCTTTGGCTCTGCTCCCC 2279 Db 2291 CGGGAGGAATTGGGAAGAAGATGGCCTGAGTGTGCACTTTGGCTTGCTACCTGCTCC 2279 Db 2280 TGAAGCCCGGCTAAAAATAATTCATCCAAGATTCCTTTGTAGTTAAAAGGGTCCAGTTCTG 2339 Db 2351 TGAAGCCCCGCTAAAAATAATTCATCCAAGATTCCTTTGTAGTTAAAAGGGTCCAGTTCTG 2410 C340 ACTGGAGCCTCTAGAAATCATCCAAGATTCCTTTTGTAGTTAAAAGGGTCCAGTTCTG 2410 C341 ACTGGAGCCTCTAAGAAGCTGGGCTTGTATTTTGGCCTTTTTGTTCCTACATAAAT 2410		Mα	US-10-108-260A-1658 Query Match Best Local Similarity 99.4%; Pred. No. 0; Matches 1232; Conservative 0; Mismatches 7; Indels 0; Gaps 0; Oy 1 AGCACGTCCCACTCTATGACCAGTGGGAGGATGATGAAAGGGATGAAGGTGGAGGTGC 60	QY 121 CAGGGTATCGGGTGCTTCGGTATGAAGGCTTTGAAATGACGCCAGCCA
CATGAAGCTGGAGCCCTGATGGAGCCCCGGCTCATCTGTGTGGCC	1331 ACAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATCCCGCCCCTAAGAGG 1390 1320 CGACCCCTCAGACAGAGGTCCAAGAAGCCCTGCTGGAGGACCTCAGGGTGCCAGG 1379 1391 CGACCCCTCAGACAGGGGTCCAAGAAGCCCTGGCGGTGCGTGC	ATCAAGCAGAAACAGACGACTGAGCCTTCCTGCCTCCAGCCTTCTAGCTGGAAGC	1740 CCGCCTGAGGCCCCAGAACTCGTCGTCGTCGACACTTTTCCAGCCAG	1991 ĠĊĊTĠAĂĊĠĀĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION UNMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PRILNG DATE: 2000-03-24
PRIOR PRILNG DATE: 2000-02-24
PRIOR PLING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARR: FABSERQ for Windows Version 4.0
SSETWARR: FABSERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-70682
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US-10-027-632-70682
US-10-027-632-70682
Sequence 70682, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Query Match 20.0%; Score 512.2; DB 13; Length 513; Best Local Similarity 99.6%; Pred. No. 1e-147; Matches 511; Conservative 2; Mismatches 0; Indels 0;
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Publication No. US20030204075A9
GENERAL INFORMATION:
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             CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR PLILNG DATE: 2000-03-39
PRIOR PLILNG DATE: 2000-03-29
PRIOR PLILNG DATE: 2000-03-29
PRIOR PLILNG DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PLILNG DATE: 2000-02-24
PRIOR PLILNG DATE: 3999-11-23
PRIOR PLILNG DATE: 1999-03-28
PRIOR PLILNG DATE: 1999-03-28
PRIOR PLILNG DATE: 1999-03-28
PRIOR PLILNG DATE: 1999-03-28
PRIOR PLILNG DATE: 1999-03-28
PRIOR PLILNG DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 325720
SOFTHARE: PRESED FOR WINDOWS VERSION 4.0
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Best Local Similarity 99.6
Matches 511; Conservative
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US-10-027-632-70682
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US-10-027-632-70683
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LENGTH: 513
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Pred. No. 1e-147;
2; Mismatches 0; Indels 0;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-3
PRIOR PILING DATE: 1999-10-3
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-3
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SECTION OF 06633
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Best Local Similarity 99.6%;
Matches 511; Conservative
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US-10-027-632-70683
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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Query Match
Best Local Similarity 99.6
Matches 470; Conservative
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; ORGANISM: Human
US-10-027-632-293974
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.0%; Score 512.2; DB 14; Length 513; Best Local Similarity 99.6%; Pred. No. 1e-147; Matches 511; Conservative 2; Mismatches 0; Indels 0;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR PLING DATE: 2002-04-30
PRIOR PLING DATE: 2002-04-30
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PRING DATE: 2000-03-29
PRIOR PRING DATE: 2000-03-24
PRIOR PRING DATE: 2000-02-24
PRIOR PLING DATE: 1999-10-23
PRIOR PLING DATE: 1999-10-23
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PRIOR PLING DATE: 1999-10-28
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US-10-027-632-70683
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PUBLICATION NO. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Sing-
TITLE DE INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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4.9e-135;
THIE REPERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRICK APPLICATION NUMBER: US 60/218,006
FRICK APPLICATION NUMBER: US 60/218,006
FRICK APPLICATION NUMBER: US 60/198,676
FRICK FILING DATE: 2000-04-20
FRICK FILING DATE: 2000-03-29
FRICK FILING DATE: 2000-03-29
FRICK FILING DATE: 2000-02-24
FRICK APPLICATION NUMBER: US 60/185,218
FRICK FILING DATE: 2000-02-3
FRICK APPLICATION NUMBER: US 60/165,358
FRICK FILING DATE: 1999-11-23
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-28
FRICK FILING DATE: 1999-09-09
FRICK FILING DATE: 1999-08-09
NUMBER OF ESC ID NOS: 325720
SOFTWARE: FRAEESC FOT WINDOWS VERSION 4.0
SSOFTWARE: FRAEESC FOT WINDOWS VERSION 4.0
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99.6%; Pred. No. 4.9
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CURRENT APPLICATION NUMBER: US/10/027,632
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PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR PRIOR DATE: 2000-02-24
PRIOR PRILICATION NUMBER: US 60/167,363
PRIOR PRILICATION NUMBER: US 60/156,358
PRIOR PRILICATION NUMBER: US 60/156,358
PRIOR PRILING DATE: 1999-09-28
PRIOR PRILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 700 29374
LENGTH: 472
            FILING DATE: 2000-04-20
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US-10-027-632-302414
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US-10-027-632-293974
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 225720
SOFTWARE: FASTSEQ FOR WINGOWS VERSION 4.0
SERIGHARIE: PASTSEQ FOR WINGOWS VERSION 4.0
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ORGANISM: Human
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1480 TGCCTGTCTCCGTCGAGAACATCAAGCAGGAAACAGACGACTGAGCCTTCCTGCCTCCAG 1539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TGACTTTGGCTTGGAGACTGATCTCTCTCTGTGTAAATTCTGCCCGGTGTGAAGGCTG 180
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GENERAL INFORMATION:

GENERAL INFORMATION:

JAPPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: 108017.129

CURRENT APPLICATION NUMBER: 105/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR PELLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218
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18.4%; Score 471.2; DB 14; Length 472; 99.6%; Pred. No. 4.9e-135; tive 2; Mismatches 0; Indels 0;
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us-10-031-915-90.rnpb

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; LOCATION: (1)...(492)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-22234
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Pred. No. 4.9e-135;
2; Mismatches 0; Indels 0;
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US-09-918-955-22234

i Sequence 22234, Application US/09918995

i Publication No. US20030073623A1

i GENERAL INFORMATION:

i APPLICANT: Hyseq, Inc.

i TITLE OF INVENTION:

i TITLE OF INVENTION: FROW VARIOUS CDNÄ LIBRARIES

i TITLE OF INVENTION: FROW VARIOUS CDNÄ LIBRARIES

i TITLE REFRENCE: 20411-756

i CURRENT APPLICATION NUMBER: US/09/918,995

i CURRENT APPLICATION NUMBER: US/09/235,076

i PRIOR APPLICATION NUMBER: US/09/235,076

i ROWNER OF SEQ ID NOS: 38054

i SOFTWARE: FREESE OF ET Windows Version 3.0

i ENCORT.
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-8

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 472
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Best Local Similarity 99.6%;
Matches 470; Conservative
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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; ORGANISM: Human
US-10-027-632-302414
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Fatent No. US20020064855A1
GENERAL INFORMATION
FAPLICANT: Lemischka, Ihor
TITLE OF INVENTION: GENES THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: CELLS AND USES THEREOF
FILE REPERBNCE: 2275-1-005
FILE REPERBNCE: 2275-1-005
CURRENT APPLICATION WUMBER: US/09/789,919
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55
LENGTH: 3590
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                                                                                     Length 492;
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                                                                           Query Match
17.1%; Score 438; DB 11; L
Best Local Similarity 100.0%; Pred. No. 9.6e-125;
Matches 438; Conservative 0; Mismatches 0;
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; ORGANISM: Mus musculus
US-09-789-919-55
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990 CTCTCGTTCCTCCTAGAACTGTTCAACATAAATATACAAACTGGAAAGCTTTTCTAGTAA 1049
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870 caddinarardcccirrigadarardaaddarrigaaardaarcrcrcgaacricr
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Search completed: February 4, 2004, 20:27:14 Job time: 892 secs 1929 GATATCAACTACAGCCTCCAG 1949 셤

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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ALIGNMENTS

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COCUS	BC023933 3441 bp mRNA linear HTC 23-SEP-2002
DEFINITION	r to
	IMAGE:5325131, mRNA.
ACCESSION	BC023933
/ERSION	BC023933.1 GI:23271699
CEYWORDS	HTC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 3441)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (05-FEB-2002) National Institutes of Health, Mammalian
	Gene Collection (MGC), Cancer Genomics Office, National Cancer
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
	USA
REMARK	NIH-MGC Project URL: http://mac.nci.nih.gov
COMMENT	Contact: MGC help desk
	Email: cgapbs-r@mail.nih.qov
	Tissue Procurement: Jeffrey Green M.D.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: National Institutes of Health Intramural

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Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Web Site: http://www.nisc.nih.gov/
Achter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Hansen,N.L., Granite,S., Ghan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Peargoon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 56 Row: o Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: frame shifted.
Location/Qualifiers
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Pred. No. 6e-273;
0; Mismatches 204; Indels
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Best Local Similarity 86.5%;
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Submitted (16-701.2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (ETKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegescriken.go.jp, PRL: Asx: 81-45-503-922, CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to
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Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
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86.4%; Pred. No. 3.4e-272;
ive 0; Mismatches 206; Indels 7;
      Bono, H.,
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Location/Qualifiers
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                                                                    AK029115

Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732493N06 product:H-L(3)MBT-LIKE PROTEIN (HYPOTHETICAL 79.1 KDA PROTEIN) homolog [Homo saplens], full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to Prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full.length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3422)
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Nature 409 (6821), 685-690 (2001)
21085660
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AACGGCTGGTGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGGAG 360
                                                                                       /note="unnamed protein product; H-L(3)MBT-LIKE PROTEIN (HYPOTHETICAL 79.1 KDA PROTEIN) homolog [Homo sapiens] (SPTR|Q969R5, evidence: FASTY, 90.9%ID, 100%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 CTGGGTACCGGGTGCTGCTGCGATATGAAGGCTTTGAAAATGACGCCAGTCATGACTTCT
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47.0%; Score 1200.4; DB 11; Length 3431;
Best Local Similarity 86.4%; Pred. No. 3.4e-272;
Matches 1351; Conservative 0; Mismatches 206; Indels 7;
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                                                                                                                         Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itch,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Kono,H., Adachi,J., Fukuda,S., Arawana,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Salto,T., Chazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Salto,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casvant,T., Fleischman,W., Gasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Flesole,G., Tomita,M., Wagner,I., Washio,T., Sakai,K., Okido,T., Fuzuki,R., Tomita,M., Baldarelli,R., Barshi,G., Bakai,K., Okido,T., Fuzuki,R., Anno,H., Baldarelli,R., Barshi,G., Bake,J., Boffelli,D., Boljunga,N., Pletcher,C., Pulta,M., Garibold,M., Gustinoich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbadh,C., Seya,T., Shibata,X., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L., Whishaaki,Y., Rawaji,H., Kohtsuki,S. Functional annotation of a full-length mouse cDNA collection and Hayashizaki,Y.

Nature 409 (6821), 685-690 (2001)
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Last (bases 1 to 3431)

Adachi, J. Alzawa, K., Akimura, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Haramoto, K., Hiracka, T., Hirozane, T.,
Hayashida, K., Hayatsu, N., Haramoto, K., Hiracka, T., Hirozane, T.,
Hayashida, K., Hayatsu, N., Haramoto, K., Hiracka, T., Hirozane, T.,
Ratoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kowda, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Takeda, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submittee (16-UL-201) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail:genome-resegescriken:go.jp,
URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222,
FAMN 1: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222,
FAMN 1: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222,
FAMN 1: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222,
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
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Please visit our web site for further details.
URL:http://genome.gec.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="9830123N10"
Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861
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                   ATCACCCACCTTCCGGAAGATCTACTGTGATGCCGTTCCTTACCTCTTCAAGAAGGTAC
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                                                     GAGCAGTCTACACAGAAGGCGGTTGGTTTGAGGAAGGGATGAAGCTGGAGGCCATTGACC
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/mol_type="mRNA"
/db_txref="txxxon:9606"
/db_txref="txxxon:9606"
/clone="CloBACIOZAOL"
/tissue_type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Wector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NorI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Nor I and cloned into
the Nor I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
Library was not normalized."
39 others
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BX446508 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA010ZA015-PRIME, mRNA sequence.
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Catarrhini, Hominidae, Homo.
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hor
1. (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Vell-length CDNA libraries and normalization
Unpublished
                                                              BX446508.1 GI:31031730
                                                                                                       Homo sapiens (human)
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Best Local Similarity
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                              CTTAAGATGGCCTCCCCCGGACCCGCCACGGCCCTCAGTTGCCAGGGATGGGGCCACCAC
                                                                                                       CTTCTGCCCTCCCCTGTGGAAAGGTCTATATGACGGGCCGCCTGAGGCCCCAGAACTCGT
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Mammalia; Eutheria; Primates;
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// db_xref="textoxon:9606"
// clone="CSOG002VEL"
// tissue_type="B_CELLS (RAMOS CELL LINE)"
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ALS60108 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA clone CS0DG002YE14 5-PRIME, mRNA sequence.
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Li,W.B., Gruber,C., Gessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12906251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10409.f For
Invitrogen. This sequence belongs to sequence cluster 10409.f For
Intp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG002BC07QPl&cluster=10409.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG002BC07QPl.
TGAGTGTGCACTTTGGCTCTGCTACCTGCTCCTGAAGCCCCGCTAAAAATAATTCATCCA
                                           AGAITCCTITGIAGTTAAAGGGTCCAGTTCTGACTGGAGCCTCTAGAGAGCTTGGG
                                                                                                                                                                                                                                                            103 ACACAGAACCCTCAAGAACAAGGATGACTGGAGGACACATCTAGCTGCCATTGCAA
                                                                        AGATTCCTTTGTAGTTAAAGGGTCCAGTTCTGACTGGAGCCTCTAGAGAGCTGGGCTTGT
                                                                                                                                  ATGITCITITGGCCTTTTGTTCCTACCTAAATGAAAACCATGCCTGGAGGGGCCGTGA
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Pred. No. 3.4e-196;
0; Mismatches 0; Indels
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2192 GACT-CCCATTTCCTAAAGGAAATGCCCCCGGGGGAGGA 2228
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                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
Plate: LLCM1910 row; g column: 23
High quality sequence start: 13
High quality sequence store: 3
1 (bases 1 to 1080)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:6074697"
/clone="IMAGE:6074697"
/lasue_vype="melanoric melanoma, cell line"
/lab host="DHIOB (phage-resistant)"
/clone_lib="NHH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/coch; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
                                                                                                                                                                                                                             1953
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AGENCOURT_7569887 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6074697
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792 AGCTCCCCAGGGATGTTGGGGGACCAGCTTGTCTCGGCAGCTAAGAACAGTGGACCAGGA B51
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1 (bases 1 to 900)
NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                           1834 CTCCCCCCGACCCGCCACGGCCCTCAGTTGCCAGGGATGGGGCCACCACTGTCACACTGT
                                                                                                                                                                                                                                 1894 GGAATACAAGACAGTGAACTCTGTCTGCCTGAACGAGTCATGTAAATTAAGTTCTAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapDs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov nc.n. column: 10
Plate: LLCM2290 row: n. column: 10
High quality sequence stop: 678.
Location/Qualifiers
                                                                                                                                          612 GGAATACAAGACAGTGAACTCTGTCTGCCTGAACGAGCCATGTAAATTAAGTTCTAGAGC
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laboratory of Gerald M. Rubin (University of California, Berkely) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II AT (Life Technologies). Note: this is a NIH MGC Library."
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                                                                                                                                                                            Query Match
31.1%; Score 794.6; DB 13; Length
Best Local Similarity 98.2%; Pred. No. 1.6e-176;
Matches 814; Conservative 0; Mismatches 14; Indels
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BQ927459

AGENCOURT 8822242 NIH MGC_40 Homo sapiens cDNA clone IMAGE:63814225', mRNA sequence.

RESULT 9 BQ927459 LOCUS DEFINITION

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/organism="Homo sapiens"
/mol type="MRNN"
/db xrefe"taxon:9606"
/clone="IMAGE:8381422"
/tissue type="carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: poTB7; Site 1: Xho1;
Site 2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5: adaptor: GGGACGAGG(3). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC_Library." 2 others
                                                                                     Enkaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Uppublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be futus; Mingel Illu.gov
Clone distribution: MGC Clone distribution information can be futus: LLCM3571 row: j column: 15
High quality sequence stop: 620.

Location/Qualifiers
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Best Local Similarity 96.9%; Pred. No. 8.6e-174;
Matches 809; Conservative 0; Mismatches 22;
GI:22342490
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                                                 Homo sapiens
Homo sapiens
BQ927459.1
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AGENCOURT 7592644 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6050456
5', mRNA Bequence.
BQ217463.1 GI:20398863
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   proteins
                                                                                                                                                                                                                                                                61 TCAGGGTGCCAGGAAGATCTCGTCGCAGCCTGTTCCTGGCGAGATCATTGCTGTGCGTGT
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   membrane and secreted
                                                                                      Length 893;
                                                                                                                          21; Indels
                                                                                    Score 773; DB 14;
Pred. No. 2e-171;
0; Mismatches 21;
                                    198 t
cancer genes encoding
Manuscript submitted."
                                                                                    Query Match
Best Local Similarity 96.8%;
Matches 811; Conservative (
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AGENCOURT_10735964 MAPCL Homo sapiens cDNA clone IMAGE:6722445 5',
mRNA sequence.
CA454956.
CA454956.1 GI:24905191
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6722445"
/cell_line="ZR-75-1, MCP7, SK-BR-3, MDA-MB-231, hTERT-HME1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (1885) 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nh.gov
Tisaue Procurement: Kristi A. Egland, Ira Pastan
ONA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM14285 row: c column: 21
High quality sequence stop: 691.
                     GCCTCATGTGTTGGTCCTCTGCTCCTAGCTCCCCAGGGATGTTGGGGACCCAGCTTG
                                                                                               2165 GAGCTGCTTTCTGTGTTTGTGAGGACTGACTCCCATTTCCTAAAGGAAATGCCCCCGGGG
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AUTHORS
TITLE
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602857991F1 NIH_MGC_10 Homo sapiens cDNA linear EST 20-JUN-2001

BI092956

BI092956.1 GI:14511286
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/mol_type="mRNA"
/mol_type="mRNA"
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/coll_line="MGC36"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 851)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                        GCCGTGGACCTGATGGAGCCCCCGGCTCATCTGTGTGGCCACGGTGAAACGAGTGGTGCAT
                                                                                                              541 GCCGTGGACCTGATGGAGCCCCGGCTCATCTGTGTGGCCCACGGTGAAACGAGTGGTGCAT
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LlAMI1029 row: e column: 23
High quality sequence stop: 803.
Location/Qualifiers
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29.0%; Score 739.8; DB 12;
Best Local Similarity 97.5%; Pred. No. 1.3e-163;
Matches 836; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BI092956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="melanotic melanoma".
/lab_host="DHIOB (phage-resistant)"
/clone_lib="NJH MGC 72"
/note="Organ: sKin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
Technologies."
2 246 c 253 g 164 t 2 others
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11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM1302 row: 1 column: 09
High quality sequence stop: 547.
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Pred. No. 2.1e-164;
0; Mismatches 20; Indels 8;
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/db_xref="taxon:9606"
/clone="IMAGE:6050456"
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Best Local Similarity 96.7%;
Matches 812; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1057)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                           1848 CCACGGCCCTCAGTTGCCAGGGATGGGGCCACCACTGTCACACTGTGGAATACAAGACAG
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REFERENCE AUTHORS

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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="traxon:9606"
/clone="INAGE:4581846"
/tissue_type="retinoblastoma"
/tab.host="bill08 (phage-resistant)"
/clone_lib="NIM_MGC_16"
/note="Organ: eys. Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oliqo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACRI/XhoI sites using the following 5' adaptor: GGCACRI/XhoI sites using the following 5' adaptor: GGCACRI/XhoI sites using the following 5' adaptor: GGCACRI/YhoI sites a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of Grant by a site of 
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Contact: Robert Strausberg, Ph.D.
Email: Gapber Cemail.nih.gov
Tissue Procurement. ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCN1303 row: d column: 07
High quality sequence stop: 763.

S Location/Qualifiers
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ilarity 93.4%; Pred. No. 4.5e-163;
Conservative 0; Mismatches 50;
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// mol_type="mRNA"
// mol_type="mRNA"
// db xref="texaon:9606"
// clone="IMAGE:495382"
// lab_bost="DH108 (T1 phage-resistant)"
// clone lib="NIH MGC 75"
// note="Organ: kIdney; Vector: pDNR-LIB (Clontech); Site 1:
Sfil (ggccgcccgcgcc); Site 2: Sfil (ggccgtratggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATARGGCC; 3 and 3' adaptor sequence:
S'-ATTCTAGAGGCGCGGCGCGCATG-AT(30)BN-3' (where B= A,
C, or G and N = A, C, G, or T). Average insert size 1:65
kb (range 0:5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
                                                      1906
                                                                                                                                                                              2022
                                                                                                          1907 GIGAACICIGICIGCCIGAA-CGAGICATGIAAA---ITAAGIICIAGAGCAGCICICIG 1962
                                                                                                                                                                                                                                            2082
629
                                                                                                                              660 GIGAACTCTGTCTGCCTGAACCGAGTCATGTTAACATTCAAGTTCTAGAGCAGATCTCG 719
                                                                                                                                                                                                                                                                                                                                                                                                                G400812 914 bp mRNA linear BST 12-MAR-2001
                                                                                                                                                                                                    720 AGCAGGATAAGGTCCCCTGACAGTGAGTGTGGTGGGGGGGAAGCTTCTGGCTCAAAAAT 779
                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                    600 GCCACGGCCCTCAGIIGCCAGGGATGGGGCCACCACIGIACACACIGIGGAAIACAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1330 row: k column: 07
High quality sequence stop: 782.
                                              GCCACGGCCCTCAGTTGCCAGGGATGGGGCCACCACTGTCACACTGTGGAATACAAGACA
                                                                                                                                                                        AGCAGGATAAGGTCCCCTGACAGTGAGTTGTGTGGTGGGGGGGCAGCCTCTGCCTCAAAAT
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                   GGGATGTTGGGGACCCAGCTTGTCTCGGCAGCTAAGAAGCAGT 2125
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Length 914;

Score 734.2; DB 10;

28.7%;

Query Match

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855 bp mRNA linear EST 17-OCT-2001
603181058F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245023 5',
mRNA sequence.
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                                                                                                 1 GAGAACTACTTGGAGAAGACCAAGTCGAAGCCGCTCCATCGAGACTCTTTAACATGGAT
                                                                                                                                            996 TGCCCAAACCATGGCTTCAAGGTGGGCATGAAGCTGGAGGCCGTGGACCTGATGGAGCCC
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                                                                                                                                                                                                                                1056 CGGCTCATCTGTGTGGCCACGGTGAAACGAGTGGTGCATCGGCTCCTCAGCATCCACTTT
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                      Gaps
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Pred. No. 2.Be
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Homo sapiens (human)
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VERSION
KEYWORDS
SOURCE
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="texon:9606"
/clone="InAGE:2245023"
/lab_host="DH10B"
/clone="Lib="WIH MGC_121"
/note="Organ: brain; Vector: pcWV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of fetal brains, female age 20 weeks, female age 20 weeks, and male age 20 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3:5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (InVitrogen). Research Genetics tracking code 017. Note:
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                       Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
Plate: LLAMISE row: d column: 16
High quality sequence start: 2
High quality sequence start: 2
Location/Qualifiers
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Pred. No. 4.3e-162;
0; Mismatches 16; Indels 10;
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this is a NIH MGC Library."
258 c 245 g 166 t
                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 97.0%;
Matches 833; Conservative
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Human cell cycle and proliferation protein CCYPR-36 cDNA, SEQ ID NO:90.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Probe #17615 for g Probe #25336 used Human liver single Human genome-deriv

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Minimum Maximum

Database

Result No.

Drosophila melanog Drosophila melanog

DNA encoding nove

bone marrow #17615 for g #25336 used

Rat 1(3)mbt protei Human ovarian PCR-Human 1(3)mbt prot Human 1(3)mbt prot Human mddt cDNA SE Human mddt cDNA SE

Human foetal liver Probe #9308 for ge Human brain expres

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Mouse

liver single genome-deriv foetal liver #19022 for g brain expres

Human Probe Human Human Human Probe Human Human Probe Human Human I Human I Human I Human I Human I

bone marrow #8618 for ge #12484 used

Hillman JL, Azimzai Y,

Yue H, Au-Young J, Bandman O; Baughn MR, Patterson C, Shah P; Tang YT, Lu DAM, Lal P, Yang J, WPI; 2001-112727/12. P-PSDB; AAB60488.

Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer

Claim 5; Page 190-191; 205pp; English

Sequences AAF5950-AAF59643 represent cDNAs encoding 54 human cell cycle and proliferation proteins (CCYPR), AAB60453-AAB60506.
CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR and associated with decreased expression of functional CCYPR, while CCYPR and associated with overexpression of functional CCYPR, Monoclonal or polyclonal antibodies to CCYPR may be used in enzyme-linked immunosorbent associated with compounds e.g., antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that modulate the activity of CCYPR. CCYPR nucleotides can be used to generate transgenic animal models of human disease, and can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR. Diseases which can be diagnosed, treated and prevented using CCYPR. proteins, nucleic acids, agonists or antagonists include immune, developmental and cell signalling disorders, and cell proliferative disorders including cancer. Specific examples of these disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allergies, diabetes mellitus, disorders of the menstrual cycle and infections

Sequence 2555 BP; 577 A; 709 C; 722 G; 547 T; 0 other;

100.0%; Score 2555; DB 22; Length 2555; 100.0%; Pred. No. 0; ö ö 0, Mismatches Conservative Similarity Best Local Sim. Matches 2555; Query Match

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(first entry)

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Human polynucleotide SEQ ID NO 935.
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Zhao QA,
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous siyetem, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, and as lateral sed neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and infammation, leukaemias and C.N.S disorders
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Zhang J;
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Yang Y,
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     cytostatic;
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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Pred. No. 0;
0; Mismatches
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nootropic; immunosuppressant;
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2000US-0598042.
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Best Local Similarity 99.9%;
Matches 2552; Conservative
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Wang Z, F
Zhou P,
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09-JUL-2000;
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                                                                                                                                    The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosting or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, oronnary arteriosolerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, reproductive disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's
                                                                                                                                                                                                                                                                                                                                                       Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder;
              GAAGCCCCGCTAAAAATAATTCATCCAAGATTCCTTTGTAGTTAAAGGGTCCAGTTCTGA
                                           CTGGAGCCTCTAGAGAGCTGGGCTTGTATGTTCTTTTTGGCCTTTTTGTTCCTAAATG
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCAACAGTGATGCTGCTCCCCAGCCGGGTGTACTGGATCGCCTCTGTCATCCAGACAG
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99.6%; Score 2544, D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2544; Conservative 0; Mismatches
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(HUMA-) HUMAN GENOME SCI Ruben SM WPI; 2003-029900/02 P-PSDB; ABR00141. Rosen CA,

ABZ71190-ABZ7147B represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP0029 represent the proteins they encode. ABZ71479-ABZ714 represent human secreted proteins they encode. ABZ71479-ABZ71540 represent human secreted proteins described by the secreted proteins and encompasses antibodies specific for the secreted proteins. The rectors and host cells computising a mucleic acid of the invention. The secreted proteins, nucleic acids encoding them, antibodies or antibody frequents specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliocating or preventing digestive disorders. Such conditions include disorders of the mouth, companies, stomach, small intestine, large intestine, liver, biliary tract and pancreas, and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the reatment of immune disorders, inflammation, infection, chromosome control samples, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute markers. The present sequence represents a human secreted protein-markers. The present sequence represents a human secreted protein-markers. The present sequence represents a human secreted protein-markers. New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers Claim 21; Page 834-835; 1216pp; English

Sequence 3530 BP; 815 A; 945 C; 972 G; 790 T; 8 other;

1074 1254 TGAAGTACCCCTTTAGGCAGGCATGCGGCTGGAAGTGGTGGACAGTCCCCAGGTGTCAC 1314 180 240 TCAACAGTGATGCTGTGCTCCCCAGCCGGGTGTACTGGATCGCCTCTGTCATCCAGACAG 120 300 480 TCCTAGTGCCCCCACGACCATCCATGCCAAGTTCACCGACTGGAAGGGCTACCTCATGA AACGGCTGGTGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGAGCA 895 AGCACGTCCCACTCTATGACCAGTGGAGGATGATGAAAGGGATGAAGGTGGAGGTGC GGTGCAACCTGGGAACAGTGGATGTCCACCCCATTGGCTGGTGTGCCATCAACAGCAAGA 1 AGCACGTCCCACTCTATGACCAGTGGGAGGATGTGATGAAAGGGATGAAGGTGGCTGC AACGGCTGGTGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGGA Toctadrecoccaceaccarcoareccaserroaceacrecaeceaeceaeceracerea TGAAGTACCCCTTTAGGCAGGGCATGCGGCTGGAAGTGGTGGACAAGTCCCAGGTGTCAC GCACTCGCATGGCTGTGGACACAGTAATCGGGGGTCGCCTACGGCTCCTCTACGAGG Gaps . 0 DB 25; Length 3530; 0; Indels Query Match

99.6%; Score 2544; D
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(first entry)

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antideterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                  polynucleotide SEQ ID NO 419.
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB80040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are established from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, (c) cardiovascular disorders such as myocardial schaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parastic infections.

(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parastic infections.

(E) Wote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. WiPo int/pub/published_pot_sequences.
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Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -
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                                                                                                                                                 Claim 4; SEQ ID NO 419; 2081pp + Sequence Listing; English.
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Matches 2537; Conservative
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and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                  Note: The sequence data for this patent did not form part of the printed specification.
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Matches 2376; Conservative
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Zhao QA, Zhou P, Goodrich R,
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25-ARR-2000; 2000US-0552317.
9-UUL-2000; 2000US-0598042.
19-UUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-059344.
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Human; foetal brain; foetal kidney; melanoma; testis; amygdala; gene therapy; chromosome 22q13.31-13.33; ss. Human transmembrane protein cDNA clone amy2_li14.

25-APR-2000; 2000US-199380P. 25-APR-2001; 2001WO-IB02050

fetal genetic Human cDNA sequences and clones derived from human fetal brain, kidney, melanoma, testis and amygdala cDNA libraries, useful in screening and therapy -

Claim 1; Page 128-129; 611pp; English.

arrays $^{\text{the}}$ from The present invention describes assemblages and computer readable comprising novel human cDNA sequences and clones derived from huma foetal brain, foetal kidney, melanoma, testis and amygdlaa cDNA libraries. ABA93702 to ABA9376 represent human cDNA sequences from present invention which encode the proteins given in ABB0562 to ABB05729. The human cDNA sequences and clones can be used in gene therapy. The clones may be used in a variety of applications, for example they may be used in profiling assays, for providing large of human genetic material for implementing large-scale screening strategies and for treating diseases via gene therapy procedures.

1610 CGAAAGCCGCTCCATCGAGACTCTTTAACATGGATTGCCCAAACCATGGCTTCAAGGTGG 1669 1021 GCATGAAGCCGCGAGACCTGATGGACTCGACTCTGTGTGGCCACGGTGA 1080 1670 GCATGAAGCCGTGGACCTGATGGAGCCCCGGGTCATCTGTGTGGCCACGGTGA 1729 1081 AACGAGTGGATGGACCTCCAGCATCCACTTTGACGGCTGGTGGGCACGGGTACGACG 1730 AACGATGGTGCATCGGCTCCTCAGCATCTACACCTGGGACAGGAGTACGACC 1789 1141 AGTGGGTGGACTCCCAGACATCTACCCCGTCGGCTGGTGGAGTACGACC 1789 1150 AGTGGGTGGACTCCCAGACATCTACCCCGTCGGCTGGTGTGAGCTCACCGGCT 1200 1161 AGTGGGTGGACTCCCAGACATCTACCCCGTCGGCTGGTGTGAGCTCACCGGCT 1200 1161 AGTGGGTGCACTCCTGTGTGGCGCTCACCCGTCGGTGTGAGCTCACCGGCT 1200 1201 ACCAGCTCCAGCTCCTGTGTGGCGCTCACCGGCTTGAGCTCCACCGGCT 1200 1204 ACCAGCTCCAGCTCCTGTGTGGCGCTCCTGGCTGGTGTGAGCTCTGAC 1909 1205 ACCAGCTCCAGCTCCTGTGTGGCGCAGTGTGGGCTCTGAC 1909 1206 ACCAGCTCCAGCTCCTGTGTGGCGCAGTGTGGGCTCTGAC 1909 1207 ACCAGCTCCAGCTCCTGTGTGGCGCTCTGAC 1909 1207 ACCAGCTCCAGCTCTGTGTGGCGCTCTGAC 1909 1207 ACCAGCTCCAGCTCTGTGTGGCCTCTGAC 1909	TTTCTTTCCTCTTTTTTTCCTTCTTCCCCCGCCCCTGTGCCCATCTCCGTTCTTTGGC ATGAGGTGGAGATGTCTCATGGACCACTTTAAGTAGAGAGTGAGCCCCGTCACCCAGCCC ATGAGGTGGAGATGTCTCATGGACCACTTTAAGTAGAGAGGTGAGCCCCGTCACCTACCT	1225		1381 AGATCTCGTCGGAGCTTCCTGGCGAGATCATTGCTGTCGTGTGAGGAAGGGATC 1440
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Sequence 3071 BP; 666 A; 882 C; 858 G; 665 T; 0 other; Query Match Best Local Similarity 79.8%; Pred. No. 0; Matches 1930; Conservative 0; Mismatches (r. 9); Indels 480; Gaps 1; Matches 1930; Conservative 0; Mismatches (r. 9); Indels 480; Gaps 1; Oy AGCACTCCACTCTATGACGAGGGAGGATGAGGATGAGGATGAGGTGC 60 Indel	Oy 241 TCCTAGTGCAACAGTGGATGTCCACCCCATTGGCTGGTGTGCCATCAACAGCAAGA 240 B30 GGTGCAACCTGGGAACAGTGGATGTCCACCCCATTGGCTGGTGTGCCATCAACAGCAAGA 889 Oy 241 TCCTAGTGCCCCACGGACCATCATGCCAAGTTCACCGACTGGAAGGGCTACCTGATGA 300 Db 890 TCCTAGTGCCCCCACGGACCATCATGCCAAGTTCACCGACTGCAAGGGCTACCTCATGA 349 Oy 301 AACGGCTGGTGGCCCCACGGACCATCCATGCCAAGATTCCACATCAAGATGGTGAAGAGCA 360 OC AACGCTTGCTACATCAAGACTTCCCGTGGATTTTCCACATCAAGATGGTGAAGAGCA 109	361 TGAAGTACCCCTTTAGGCAGGCATGCGGCTGGAAGTGGTGACACAGTGCTCAGGTGTCAC 1010 TGAAGTACCCCTTTAGGCAGGCATGCGGCTGGAAGTGGTGACACAGTGCTCAGGTGTCAC 421 GCACTCGCATGGGTGAACAGAAATCGGGGGTTCACAGGTTCACAGG 421 GCACTCGCATGGCTGAAGAAATCGGGGGTTCACAGGGTCCTCTACAGG 481 ATGGTGACGTGACGACACAGAATCGGGGGTTCATAGGCTCCTCTACAGGG 481 ATGGTGACAGTGACGACTTCTGGTGCCAATGTGAAGACCCCTGAAGAGGG 482 ATGGTGACAGACGACTTCTGGTGCCAATGTGAAGACCCCTGATCCACCCAGTGG 483 ATGGTGACAGTGACGACGACTTCTTGATGAAGACCCCCTGATCCACCCAGTGG 484 ATGGTGACAGACGACGACTTCTTGATGAAGACCCCCTGATCCACCCAGTGG 485 ATGGTGACAGACGACGACATTCTGATGAAGACCCCCTGATCCACCCAGTGG	541 GTTGGTCACGACGTCACGGCATCAAGATGTCAGAGAGGCGAAGTGACATGGCCC 541 GTTGGTCACGACGTGTCGGCAACGACATCAAGATGTCAGAGAGGCGAAGTCACATGGCCC 611 ATCACCCCACCTTCCGGAAGATCTCTGTGATGCCGTTCCTTACCTCTTCAAGAGGTAC 601 ATCACCCCACCTTCCGGAAGATCTACTGTGATGCCGTTCCTTACCTCTTCAAGAGGTAC 601 ATCACCCCACCTTCCGGAAGATCTACTGTGATGCCGTTCCTTACCTCTTCAAGAAGGTAC 601 GAGCAGTCTACACAGAAGATCTACTGTGATGCCGTTCCTTACCTCTTCAAGAAGGTAC 601 GAGCAGTCTACACAGAAGGCCGTTGGTTTGAGGAAGGATCCTTTCAAGAGGCCATTGACC 61 [

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Best Local Similarity 60.2
Matches 735; Conservative
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                                                                                                                                                 Hematopoietic stem cell signaling proteins modulating replication and differentiation for treating immune system disorders and leukaemia -
                     TCCTCTCTGTGTAAATTCTGCCCGGTGCTGTGAAGCTGGACGGTGGAGGAGGACGTGGAGCTGGGG
                                                            2810 Grerecrissalecesecratriserrecerecereceteresalassereraransasses
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                                                                                                                                                                                                                                                                                                                                                                                         aa:Val)
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                                                                                                                                                                                                                                                                                                                     Haematopoietic stem cell; immune system disorder;
leukaemia; antileukaemic; immunomodulator; therapy;
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primitive HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins (see AAY79176-93) are growth factors, transcription factors, splicing factors, capping factors transport proteins, translation factors or replication factors that modulate HSC activity, especially differentiation or replication. The invention provides a claimed method for identifying PHSC-specific nucleic acids involving: creating a PHSC cDNA library and a non-PHSC immune cell library; and subtracting the 2 libraries. Also claimed are methods: for generating a stem cell/progenitor cell-from PHSCs; for identifying the presence of a PHSC in a sample; for identifying the presence in a sample of a compound that modulates HSC activity; for using such a compound to creat an immune system condition, especially leukaemia; for introducing exogenous nucleic acid into a HSC; and for ex vivo expansion of HSCs. Also claimed is a PHSC specifically expressing 1 ceptanied nucleic acids, such as the present sequence.
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detecting an angiogenesis-associated transcript in a cell in the pratient. The method involves contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence at least 80% identical to any of the angiogenesis-associated human polymucleotide sequences given in the specification. These angiogenesis-associated polymucleotide sequences comprise genes that exhibit changes in expression levels as a function of time in tissue cundergoing angiogenesis. The method and the polymucleotide sequences of the invention are useful for diagnosing and treating angiogenesis and angiogenesis-associated diseases e.g. cancer. The polymucleotide sequences are also useful in the gene therapy of such disorders. The angiogenesis-associated proteins encoded by the polymucleotide caquences are useful as a vaccine for therapeutic and prophylactic immunisation. ABX08739-ABX08853 represent angiogenesis-associated immunisation.
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changes in expression level as a function of time in tissue
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                                                                                                                                   compositions for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2564 BP; 832 A; 482 C; 560 G; 690 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 405.2; DB 25;
Pred. No. 1.3e-101;
0; Mismatches 453;
                                                                                                                                   to methods and
                                                                                  291pp; English
                                                                                                                                         invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.2%;
Matches 721; Conservative
                                                                                  Page 274-275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide sequences.
                                undergoing angiogenesis
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                                                          ACCTGATGATCTGTGGACGGGGGCCCTCCACAGATGGCTTGGACTGGTTCTGCTACC
                                                                                                                                                                       ATGCCTCTTCCCACGCCATCTTCCCGGCCACCTTCTGTCAGAAGAATGACATTGAGCTCA
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angiogenesis-associated disease; cancer; cytostatic; gene therapy;
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19-ARK-2001; 2001US-285475P.
03-AUG-2001; 2001US-310025P.
13-NOV-2001; 2001US-354666P.
29-NOV-2001; 2001US-334244P.
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P-PSDB; ABU03557.
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                                                                                                                801 GGGCCCTCCACAGATGGCTTGGACTGGTTCTGCTACCATGCCTCTTCCCACGCCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polymucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ovarian cancer related cDNA clone SEQ ID NO:701
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polypeptide encoded by a polymucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II).

(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's bloidgical sample professed in a patient with (IV), detecting the amount of polymucleotide hybridising to (IV), and comparing the amount to patient where the amount of polymucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PRR). (I) comprising catected preferably by polymerase chain reaction (PRR). (I) comprising contecting for an ovarian tumour protein comprising contacting T cells with (III) or (II) is useful for stimulating and/or expanding T cells with (III) or (III) is useful in design and preparation of the tumour polypeptides and proteins in tumour cells and to isolate a full length gene from a contacting term of contacting the contacting to contact the contact of the tumour polypeptides and proteins in tumour cells, and to isolate a full length gene from a contact of the contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of contact of 
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stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2339 GACTGGAGCCTCTAGAGGCTGGGCTTGTATGTTCTTTTGGCCTTTTTGTTCCTACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2399 TGAAGAAACCATGCCTGGAGGGGCCGTGAACACAGAACCCCTCAAGACAAAGATGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 TGAAGAAACCATGCCTGGAGGGCCGTGAACACACAGAACCCTCAAGACAAGAACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2459 CIGGAGGACACAICIAGCIGCCAITGCAACCICACIGGGCICCCCAGACICIGIGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 CCGGGGAGGACATTGGGAAGAAGATGGCCTGAGTGTGCA------CTGCTACCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2279 CIGAAGCCCCGCTAAAATAATICAICCAAGAITCCITIGIAGITAAAGGGICCAGTICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 CTGAAGCCCCCCCTAAAAATAATTCATCCACAAGANTCCTTTGTAGTTAAAGGGTCCAGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 476 BP; 116 A; 124 C; 117 G; 112 T; 7 other;
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12.7%;
Best Local Similarity 95.5%;
Matches 358; Conservative (
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Best Local Similarity
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treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarchinoma, carcinnema, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, aguamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                  RESULT 12
AAH87128/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (given in ABL61664 expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent which result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endress G, Horrigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 7266; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carter KC,
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26-SEP-2000; 2000US-235637P.
26-SEP-2000; 2000US-235638P.
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27-SEP-2000; 2000US-235711P.
27-SEP-2000; 2000US-235720P.
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Weaver Z;
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                                                                                                                                                                                                                                                                                                                                          CTGGGACAGCGAGTACGACCAGTGGGACTGCGAGTCCCCCAGACATCTACCCCGTCGG
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                                                                                                                                        1001 AAACCATGGCTTCAAGGTGGGCATGAAGCTGGAGGCCGTGGACCTGATGGAGCCCCGGCT
                                                                                                                                                                                                                                            1061 CATCTGTGTGGCCACGGTGAAACGAGTGGTGCATCGGCTCCTCAGCATCCACTTTGACGG
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                                                                                                                                                                                             1 AAACCATGGCTTCAAGGTGGGCATGAAGCTGGAGGCCGTGGACCTGATGGAGCCCCGGCT
                                                                                                 Gaps
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/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 281.4; DB 24; Length 418; Pred. No. 1.2e-67; 0; Mismatches 8; Indels 0;
Sequence 418 BP; 103 A; 112 C; 124 G; 76 T; 3 other;
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replace(126, A)
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                                               Query Match
Best Local Similarity 97.3%;
Matches 285; Conservative
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Variation
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             This invention describes novel human nucleic acid segments (I) containing polymorphic sites. The polymucleotides of (I) are used for, e.g. correlating disease polymorphisms (or disease succeptibility) or other phenotypic traits (e.g. baldness, obssity, fertility, strength, response to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation, heart or central nervous system diseases; detecting susceptibility to microbial infection; treating or preventing such diseases; forensic analysis; gene therapy; paternity testing; mapping genomic loci associated with phenotypic traits (and subsequent cloning
                                                                                                                                                        of the genes responsible), and the production of transgenic organisms. Antibodies raised against (I) are useful as diagnostic and therapeutic tools and in drug screening. AAH85144 - AAH87644 represent the human DNA sequences containing blailelic polymorphic sites described in the
                                                                                                                                                                                                                                                                                                                                                 2180 TTTGTGAGGACTGACTCCC--ATTTCCTAAAGGAAATGCCCCCGGGGGAGGACATTGGGAG
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                                                                                                                                                                                                                                                  Sequence 289 BP; 72 A; 77 C; 68 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                  Score 271.8; DB 20;
Pred. No. 4.6e-65;
0; Mismatches 2;
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98.6%;
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Matches 285;
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                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                             relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                     Score 266.4; DB 23; Length 3486;
Pred. No. 5e-63;
0; Mismatches 501; Indels 41;
                                                                        Claim 1; SEQ ID NO 34672; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                 Sequence 3486 BP; 939 A; 901 C; 869 G; 777 T; 0 other;
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                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                      Sequence 4379 BP; 1162 A; 1151 C; 1118 G; 948 T; 0 other;
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10.4%; Score 266.4; DB 23;
Best Local Similarity 55.6%; Pred. No. 5.5e-63;
Matches 678; Conservative 0; Mismatches 501;
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RESULT 15

AAT23623 standard; cDNA to mRNA; 290

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AAT23623

05-SEP-1996

Human gene signature HUMGS05481.

signature; messenger RNA; mRNA; relative abundance; frequency; human, cloning, mapping, non-biased library, diagnosis, detection, cell typing, abnormal cell function, ss. Gene

sapiens Homo W09514772-A1

01-JUN-1995

94WO-JP01916 11-NOV-1994; 93JP-0355504 12-NOV-1993;

(MATS/) MATSUBARA K. (OKUB/) OKUBO K.

Okubo K; Matsubara K,

WPI; 1995-206931/27

Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues

Claim 1; Page 1414; 2245pp; Japanese

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mNA is Claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the

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3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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9.9%; Score 252.8; DB 16; Length 290;
Best Local Similarity 92.7%; Pred. No. 8.6e-60;
Matches 268; Conservative 0; Mismatches 20; Indels 1;
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AX078286 Sequence AJ305226 Homo sapi	BC017191 Homo sapi	AX714233 Sequence AK056443 Homo sapi	AJ305227 Homo sapi	AK074091 Homo sapi AL136564 Homo sapi	AK097052 Homo sapi	ALO30864 Mus muscu ALO35681 Human DNA	AY237001 Mus muscu	AY237002 Mus muscu BD115452 EST and e	AX046388 Sequence	BC020018 Mus muscu AK000062 Homo sapi	G14475 human STS S	AX336757 Sequence G43605 WIAF-2484-S	BT006011 Drosophil	G14931 numan STS S AC101996 Mus muscu	AC102262 Mus muscu	AC109565 Rattus no	AC009200 Drosophil	AC010214 Drosophil	BX088589 Danio rer	AX209757 Sequence	BC0398Z0 HOMO BAPI IR9358 Human 1(3)m	AB014581 Homo sapi	AC099875 Mus muscu	AL110279 Homo sapi	AC099875 Mus muscu	ACOUSESS HOMO SAPI BC012882 Homo sapi	BC048421 Homo sapi	BC040188 Homo sapı ax156560 Secmence	ECO36972 Mus muscu	AB032165 Mus muscu		linear PAT 22-FEB-2001			Vertebrata; Euteleostomi; i; Hominidae; Homo.	Young, J.,	Patterson, C	
SUMMARIES	Ħ	AX078286 HSa305226						_	0	0		0	-	_	4	_									-	_					10 BC036972	0	ALIGNMENTS	2555 bp DNA Patent WO0107471.	57977	(r	; Chordata; Craniata; V ; Primates; Catarrhini;	, Tang, Y.T., Yue, H	Lu, D.A., Baughn, M.R. feration proteins	
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FSKTKRPCSVSCSRSYSSNSKKASILARLQGKPPTKKAKVLHKAAMSAKIGAFLHSQC
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alternative splicing; H-1(3)mbt-like gene; H-1(3)mbt-like protein.
Homo sapiens (human)
Homo sapiens
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Homo sapiens mRNA for H-1(3)mbt-like protein, alternative variant
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                         GACAGTGAGTTGTGTGGGGGGGGGCGTCTGCCTCAAAATTCACCAAGCAGAATGCCT
                                                                                                                                                                                                                        CTTGTCTCGGCAGCTAAGAAGCAGTGACCAGGATGTGGATTTTTGGCGACCTGTGTGGTGG
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                                                                                                                        CTCAGCCTCATGTGTTGGTCCTCTGCTCCTAGCTCCCAGGGATGTTGGGGACCCAG
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Molecular characterization of h-l(3)mbt-like: a new member of human mbt family
PEBS Lett. 507 (1), 119-121 (2001)
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/map="22q13.31-33"
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AACGGCTGGTGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGAGCA
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                                                                   TCCTAGTGCCCCCACGGACCATCCATGCCAAGTTCACCGACTGGAAGGGCTACCTCATGA
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                         GGTGCAACCTGGGAACAGTGGATGTCCACCCCATTGGCTGGTGTGCCATCAACAGAAA
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                                                                                                                                                                                                                                       Web site: http://www.nisc.nih.gov/
Contact: nisc_mg/conhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,B., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAL Plate: 4 Row: b Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mkNA gi: 13899349. Location/Qualifiers
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                     cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-römail.nih.gov
Tissue Procurement: ATCC
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Db 2988 TIGGAGCTCTAGAGAGCTGATGTTCTTTTGCCTTTTTGTTCCTACCTA	RESULT 4 AX714233 LOCUS AX714233 LOCUS DEFINITION Sequence 917 from Patent EP1293569. ACCESSION AX714233 G1:29889185 ACCESSION AX714233.1 G1:29889185 SCHWORDS SOURCE ORGANISM Homo sapiens (human) CORGANISM Homo sapiens CORGANISM Homo sapiens Homo sapiens CORGANISM Homo sapiens Fultaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE SOURCE AUTHORS I sogai, T.; Sudiyama, T.; Otsuki, T.; Wakamatsu, A.; Sato, H.; Ishii, S.; Yamamoto, J. I.; Isono, Y.; Hio, Y.; Otsuka, M.; Nagai, K.; Irie, R.; Tamechika, I.; Seki, N.; Yoshikawa, T.; Otsuka, M.; Nagahari, K. and	Masubo, Y. Full-length cDNAs JOURNAL Patent: EP 1293569-A 917 19-MAR-2003; Helix Research Institute (JD) - Research Association for Helix Research Institute (JD) - Research Association for Biotechnology (JP) FEATURES 1. 3188 / crganism="Homo sapiens" / mol_type="genomic DNA" / db_xref="texon:9606" BASE COUNT 725 a 869 c 909 g 685 t	Query Match 99.4%; Score 2538.8; DB 6; Length 3188; Best Local Similarity 99.9%; Pred. No. 0; 0 0 Adchastrative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 AGCACGTCCCACTCTATGACCAGTGGGAGGATGAAAGGGATGAAGGAGGATGC 60 60 647 AGCACGTCCCACTCTATGACCAGTGGGAGGATGAAGGATGAAAGGTGGAGGTGC 706	Oy 61 TCAACAGTGATGCTCCCCCAGCCGGGTGTACTGGATCGCCTCTGTCATCCAGACAG 120	Oy 181 GGTGCAACCTGGGAACAGTGGATGGCCCCATTGGCTGTGTGCCATCAACAGCAAGA 240 Db 827 GGTGCAACCTGGGAACAGTGGATGTCCACCCCATTGGCTGTGTGCCATCAACAGCAAGA 886 Qy 241 TCCTAGTGCCCCCACGGACCATCCATGCCAAGTTCACCGGTGGAAGGCTACTCATGA 300 Db 887 TCCTAGTGCCCCCACGGACCATCCATGCCAAGTTCACCGACTGGAAGGCTACTCATGA 300 Oy 301 AACAGTGCCCCACGGACCATCCCATGCCAAGTTCACCGACTGGAAGGGCTACTCATGA 946 Oy 302 AACAGCTGGTGGGCTCCAGGACGTTCCCGTGGATTTCCACATCAAGATGGTGGAAGGCA 1006 Oy 347 AACAGCTGGTGGGCTCCAGGACGTTCCCGTGGATTTCCACATCAAGATGGTGGAAGGCA 1006	100 Tobaco (1000)
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Fukuzumi,Y., Sato,H., Wakamateu,A., Ishii,S., Yamamoto,J., Irie,R.,
Ctsuki,T., Sato,H., Wakamateu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Satio,K., Nishikawa,T., Kimura,K., Yamamahita,H.,
Matsuo,K., Makamura,Y., Sehine,M., Kikuchi,H., Kanda,K.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T., Sugano,S.,
NEDO human cDNA sequencing project
Inpublished
I cogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
Direct Submission
Submitted (24-0cT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mailigenomicsahrin,co.jp, Telis,438-52-3975, Fax:81-438-52-386)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan, construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB,
HRI, and Bictechnology Center, National Institute of Technology and
Evaluation, clone selection for full insert sequencing: RAB and
HRI.
                                          AKO56443 3188 bp mRNA linear PRI 01-AUG-2002 Homo sapiens cDNA FLJ31881 fis, clone NT2RP7002829, weakly similar to Scm-related gene containing four mbt domains.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2"
/clone_lib="NT2"
/clone_vor cells after 5-weeks retinoic acid (RA)
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Pred. No. 0;
0; Mismatches 2;
                                                                                               AKO56443.1 GI:16551846
Oligo capping; fis (full insert sequence).
Homo capiens (human)
Homo sapiens
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/organism="Homo sapiens"
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3047 AAGAAACCATGCTGGAGGGCCGTGAACACAGAACCCTCAAGAAGAAGATGACAGAGGT 3106
                                                     HSA305227 3299 bp mRNA linear PRI 18-JAN-2002 Homo sapiens mRNA for H-1(3)mbt-like protein, alternative variant
                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-JAN-2001) Wismar J., Johannes Gutenberg Universitaet,
Institut fuer Genetik, Becherweg 32, 55099 Mainz, GERMANY
Location/Qualifiers
                                                                                                                                                                                                        A3305227.1 GI:13940240
alternative splicing, H-1(3)mbt-like gene; H-1(3)mbt-like protein.
Homo sapiens (human)
Environment
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Best Local Similarity 96.0%; Pred. No. 0;
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Matches 2538; Conservative
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Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research
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Homo sapiens mRNA for FLJ00162 protein.
AK074091
AK074091. GI:18676529
fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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The nucleotide sequence of a long cDNA clone isolated from
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/db_xref="taxon:9606"
/clone="FL100162"
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Wienann, S.

Direct Submission

Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152

Direct Submission

Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152

Martinsried, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKE2): Email s.wiemannGekfz-heidelberg; de;

sequenced by MediGenomix (Martinsried/Germany) within the CDNA

sequencing consortium of the German Genome Project. This clone

(DKE2PD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available

at http://mips.gsf.de/proj/cDNA/.
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SKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESWKYPFRQGMRLEVVDK
SKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESWKYPFRQGMRLEVVDK
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CKVILLDGYLMICVDGGSTDCLDWFCYHASSFAIFPRFCQKNDIELPPRGYSRAQTF
NWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLL
                                                                                                                                                                                                                                             Homo sapiens mRNA; cDNA DKFZp7611141 (from clone DKFZp7611141); complete cds.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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DH10B; sites NotI + SalI"
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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                       480; Gaps
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1670 GCATGAAGCTGGACCTGGACCTCGGCTCATCTGTGGCCACGGTGA 1729 1081 AACGAGTGCATCGCTCCTCAGCATCCACTTTGACGGCTGGGACGGCAGTACGACC 1140	CTGCTCCTGACTTCTCTGTCCCTTTCCCTCTGGCCTGCAGAGCTCCTTCCT	2330 TCTTTCACCCTTGTCTTTCAACAACGGCCCACCCCGCTGAAGGCCCAAAGAGGCCA 2389 1261 CAAGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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Nus musculus (house mouse)

Nus musculus (house mouse)

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus musculus

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3395)

Straueberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Colline, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Riausner, R.L., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Zordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, F.J.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Bouffard, G.G., Radriguez, A.C., Grimwood, J., Schmutz, J., Weren, R.D.,

Boutfard, G.G., Radriguez, A.C., Grimwood, J., Schmutz, J., Wers, R.M.,

Butterfield, Y.S., Kazywinski, M.I., Salska, U., Sanallus, D.E.,

Bouterine, J. Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse conk, sequences
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Mus musculus RIKEN cDNA 4722493N06 gene, mRNA (cDNA clone MGC:31247
IMAGE:4211489); complete cds.
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          1559 CCTCTTCCCACGCCATCTTCCCGGCCACCTTCTGTCAGAAGAAGAAGAACATTGAGCTCACAC
                                                                                                              1619 CGCCAAAAGGTTATGAGGCACAGACTTTCAACTGGGAGAACTACTTGGAGAAGACCAAGT
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NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site:

http://www-shgc.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
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OFGKKRKRIPPSAKTRPLRQGSKKPLLEDNLEALGVSEPVPDDIIAVCVKEEHQDISSP
DRSPSPQLPLPIESIKQERNN"
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                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G B. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 43 Row: i Column: 12. This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Pred. No. 1.7e-297;
0; Mismatches 204; Indels 7;
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Best Local Similarity 86.5%;
Matches 1353; Conservative
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//gene="dd756023.1"
complement (join(<28566. .28769,29910. .30076,30602. .32311,32869. .33046,34152. .34282))
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MNDCDNHGEKVGWKLAEAVDLMEPRLLCAFUYKRVRHRLLESHBGGWDSESYDGWYDCE
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transcriptional_repressor)"
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Tr:086637"
true left end of clone RP5-979N1 is at 89849 in this sequence. T
true right end of clone RP1-85F18 is at 80441 in this sequence.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (10832, .11352)
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complement (10989, .11290)
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11441. 11790
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11455. 11594
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17446. .24698
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/note="match: STS: Em:G43605"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Em: G14931"
                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (24311. .24697)
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                                                                                                                                                                                                                                                                                                                               /map="q13.31-13.33"
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/clone="nRPC1-4"
2172. . . 2466
/note="AluSg1_repeat: ma
                                                                                                                                                                                                       /mol_type="genomic_DN
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/chromosome="22"
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United: Submission

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On May 27, 1999 this sequence version replaced gi:4775627.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

Only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em., EMBL, Sw.; SWISSERCT; Tr.; TREMBL, WD:, WORMER; Information

on the WORMERP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

has been finished according to sequence map criteria as follows.

An attempt is made to resolve all sequencing problems, such as

compressions and repeats, but not necessarily within known

annotated repeat sequence elements. Where the sequence is

anbiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of

human chromosome 22, constructed by the Sanger Centre Chromosome 22

human chromosome 22, constructed by the Sanger Centre Chromosome 22

human chromosome 22, constructed by the Sanger Centre Chromosome 22

human chromosome 22, constructed by the Sanger Centre Chromosome 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS756G23
Human DNA sequence from clone RP4-756G23 on chromosome 22G13.31-13.33 Contains the 5' part of a gene similar to drosophila transcriptional repressor, the 3' end of the gene for a novel Leucine Rich Procein, the RANGAPI gene for Ran GTPasse activating protein 1, ESTS, GSSs and three putative CpG islands, complete
                                       GACCCCTCAGACAGGGGTCCAAGAAGCCCCTGCTGGAGGACGACCTCAGGGTGCCAGGA 1380
                                                                                                                   1931 GGCCCCTCAGACAGGCCTCCAAGAAACCCTTACTGGAGGACAACCTTGAGGCTTTGGGG- 1989
                                                                                                                                                                                                            1440
                                                                                                                                                                                                                                                                                       1441 TAGACGTGGCCTCGCCCGACAAGGCTTCAAGTCCAGAGCTGCCTGTCCGTCGAGAACA 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                          2045 AGGACATTTCCTCGCCTGACAGTCGCCCAGTCCACAGCTGCCTCTTCCCATTGAGAGCA 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1501 TCAAGCAGGAAACAGACGACTGAGCCTT-CCTGCCTCCAGCCTGGCTTCTAGCTGGAAGC 1559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr22
RP4-756G23 is from the library RPCI-4 constructed by the group
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2105 TCAAGCAGGAGGAACAACTGAGACTTCCCTGGCATCAGCCTGGACCCTAACTGAAGCC
                                                                                                                                                                                                   AL035681.13 GI:4902689
HTG; CpG island; Ran GTPase activating protein; RANGAP1.
Homo sapiens (human)
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Mammalia; Butheria; Primates;
1 (bases 1 to 89948)
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HS756G23
LOCUS
DEFINITION
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TITLE
JOURNAL
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KEYWORDS
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/protein_id="CAB63073.1"
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| db_xref="SW1557273"
| db_xref="SW1557575"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTGGAATACAAGACAGTGAACTCTGTCTGCCTGAACGAGCCATGTAAATTAAGTTCTAG
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/product="dJ756G23.2 (Ran GTPase activating protein 1)
                                                                                                                                                                                                                                                                                                                                                        TCATTGCTGTGCGGTGTGAAGGAAGAGCATCTAGACGTGGCCTCGCCCCGACAAGGCTTCAA
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                                                                                                                                                                                        DB 9; Length 89948;
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0
                                                                                                                                                                                 Score 1132.4; DB 9
Pred. No. 3.3e-279;
0; Mismatches 1;
                                                                                                                                                                                    Query Match
Best Local Similarity 99.9%;
Matches 1133; Conservative
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ALAGICRLIYLYLSDNQLAGLSAAALEGAPRLGYLYLERNRFLQVPGAALRALPSLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHLQDNAVDRLAPGDLGRTRALRWYLSGNRTTEVSLGALGPARELBKLHLDRNQLRB
VPTGALEGLPALLELQLSGNPLRALRDGAFQPVGRSLQHLFLNSSGLEQICPGAFSGL
GPGLQSLHLQKNQLRALPALPSLSQLELIDLSSNPFHCDCQLLPLHRWLTGLNLRVGA
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39047. .39317
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941 AGCGGTTGGTGGGTTCCAGGACACTTCCTGCAGACTTCCATATCAAGATGGTGGAAAGCA 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    701 TCAACAGCGATGCTGTGCTCCCCAGCCGGTGTACTGGATCGCCACTGTCATCCAGGCAG 760
                                                                                                                                                                                                                                                                                                                                                                          641 AACATGTACCCCTCTATGACCAGTGGGAAGACGTCATGAAGGGGATGAAGGTGGAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCAACAGTGATGCTGTGCTCCCCCAGCCGGGTGTACTGGATCGCCTCTGTCATCCAGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 GCACTCGCATGGCTGTGGTGGACACAGTAATCGGGGGTCGCCTACGGCTCCTTACGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ATGGTGACAGTGATGACGACTTCTGGTGCCATATGTGGAGTCCCCTGATCCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1241 ATCACCCCACCTTCCGGAAAATCTACTGTGATGCTGTACCTTTACCTCTTCAAGAAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 GAGCAGTCTACACAGAAGGCGGTTGGTTTTGAGGAAGGGATGAAGCTGGAGGCCATTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1301 GCGCTGTCTACACAGAAGGTGGCTGGTTCGAGGAAGGAATGAACTAGAGCCATTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1361 crchgaarcheedcagnarcherchacaaccarchecaaeerecrtreearestrace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821 GGTGCAACTTGGGAACTGTGGATGTCCACCCCATTGGGTGGTGTGCCATCAACAGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AACGGCTGGTGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 TGAAGTACCCCTTTAGGCAGGCATGCGGCTGGAAGTGGAGAGAGTCCCAGGTGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 ATGGTGACAGTGACGACTTCTGGTGCCACATGTGGAGCCCCCTGATCCACCCAGTGG
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44.2%; Score 1128.2; DB 10
Best Local Similarity 88.9%; Pred. No. 3.9e-278;
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                                                                                                                                                        24585 CAGAACCCTCAAGACAAGGATGACAGAGCTGGAGGACACATCTAGCTGCCATTGCAACCT 24644
                                                           24525 TTCTTTTGGCCTTTTGTTCCTACCTAATGAAGAAACCATGCCTGGAGGGGCCGTGAACA 24584
                                                                                                                2490
                                                                                                                                                                                                                                                                                                                                                                          AY237001 3399 bp mRNA linear ROD 15-APR-2003
Mus musculus M4MBT variant B (M4mbt) mRNA, complete cds;
                      TICTITIGGCCTITITGTTCCTACCTAAATGAAGAAACCATGCCTGGAGGGGCCGTGAACA 2430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQVSRIRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSD
RRCDMSHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGSICVATI
CKVLLDGYLMICVDGGPSTDGSDWFCYHASSHAIFPATFCQKNDIELTPPKGYETQPF
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SIHFDGWDDRYDGWVDCESPDIYPVGWCELTGYQLQPPVSAEPNTPQKGKDTTKKKKK
QFGKKRKRIPSAKTRPLRQGSKKPLLEDNLEALGVSEPVPDDSRPVHSCLPPLRASSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 3399)
Markus,J., Feikova,S., Sramko,M., Wolff,L. and Bies,J. Cloning and molecular characterization of the novel murine gene M4mbt encoding a nuclear zinc finger protein with four mbt domains Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSKTKRFCSVSCSRSYSSNSKKASILARLQGKPPTKKAKVLHKAAWSAKIGAFLHAQG
TGQLADGTPTGQDALVLGFDWGKFLKDHSYKAAPVSCFKHVPLYDQWEDVWKGMKVEV
LNSDAVLPSRVYWIATVIQAAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAIN
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SSYLEESSEAENEDREAGELPTSPLHLFSSANNRSLDGSGSEPAVCEMCGIVGTREAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3399)
Markus, J., Felikova, S., Sramko, M., Wolff, L. and Bies, J.
Direct Submission
Submission
Submitted (14-FEB-2003) Department of Molecular Virology, Cancer
Research Institute of Slovak Academy of Sciences, Vlarska 7,
Bratislava, Slovak Republic
Location/Qualifiers
                                                                                                             CAGAACCCTCAAGACAAGGATGACAGAGCTGGAGGACACATCTAGCTGCCATTGCAACCT
                                                                                                                                                                                                                                CACTGGGCTCCCCAGACTCTGTGTGAGAAATTAAACCCCCTGCTTGAG 2544
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note="alternatively spliced"
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product="M4MBT variant B"
protein_id="AAO84917.1"
db_xref="G1:29569826"
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/gene="M4mbt"
/ntoe="R82jon: mbt repeat"
916. .1212
/gene="M4mbt"
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/mol_type="mRNA"
/strain="Swiss Webster"
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GOLADGTPTGQDALVLGFDWKFLLNDSSYRABVSCFKHUPLYDQDBDVNKGMKVEV
LNSDAVLPSRYVMTAVTOLABAGYKVLLKYEGPENDASHDFWCNLGTVDVHPIGWCAIN
SKLLVPPRTHAKFTDWKSYLMKRLVGSRTLPADFHIKMVSSMKYPFRQGMELEVVDK
TQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLTHPWGWSRRVGHGIKMSG
O"
SSYLEESSEAENEDREAGELPTSPLHLFSSANNRSLDGSGSEPAVCEMCGIVGTREAF
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Pred. No. 3.3e-211;
0; Mismatches 206;
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/gene="M4mbt"

/note="Region: putative zinc fir

580. 894

/gene="M4mbt"

/note="Region: mbt repeat"

/gene="M4mbt"

/gene="M4mbt"

/note="Region: mbt repeat"

/gene="M4mbt"
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Markus,J., Feikova,S., Sramko,M., Wolff,L. and Bies,J.
Cloning and molecular characterization of the novel murine gene Mambt encoding a nuclear zinc finger protein with four mbt domains Unpublished
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Markus,J., Felkova,S., Sramko,M., Wolff,L. and Bies,J.
Direct Submission
Submitted (14-FEB-2003) Department of Molecular Virology,
Research Institute of Slovak Academy of Sciences, Vlarska
Bratislava, Slovak Republic
Location/Qualifiers
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Catarrhini, Hominidae, Homo.
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JP 2002010789-A/7529
I15-JAN-2002
07-AUG-200 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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Location/Qualifiers
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Homo sapiens
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebr:
Mammalia; Eutheria; Primates; Catarrhini; Homin
I (bases 1 to 458)
Edvards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
Patent: JP 2002010789-A 7529 15-JAN-2002;
GENSET CORP
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